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(without alignments)
3127.023 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                 October 11, 2004, 10:08:26
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Maximum DB seq length: 2000000000
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132
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

IIES	Description	US-10-313-994-30 Sequence 30, Appl		US-10-027-632-77713 Sequence 77713,	US-10-027-632-77713 Sequence 77713,	39-386-4727 Seguence 4727, Ap	US-09-933-767-97 Sequence 97, Ag	US-10-004-860-97 Sequence 97, Appl	Seguence 97,	Seguence	US-10-369-493-33481 Sequence 33481,	JS-09-887-576-863 Sequence 863, App	US-10-437-963-37892 Sequence 37892,	17-192-1786 Sequence 1786, Ap	US-10-027-632-38125 Sequence 38125,
SUMMARIES	e e	US-10-31	US-10-31	US-10-02	US-10-02	US-10-029-386-4	US-09-93	US-10-00	US-10-02	US-10-26	US-10-36	US-09-887	US-10-43	US-10-08	US-10-02
	DB	15	15	13	16	15	10	13	15	16	16	σ	17	13	13
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	Score	132	109.2	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.2	27.8	27.8	27.2	26.8
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Sequence 38125, A Sequence 17641, A Sequence 1764, Appli Sequence 694, Appli Sequence 1417, Appli Sequence 1417, Appli Sequence 17120, A Sequence 77121, A Sequence 77121, A Sequence 77121, A Sequence 300287, Sequence 300287, Sequence 300287, Sequence 77121, A Sequence 300287, Sequence 300287, Sequence 77121, A Sequence 7	22111100011112	684, p 240, p 3, App ce 10, p ce 2058,
US-10-027-632-38125 US-10-767-701-17641 US-09-938-842A-694 US-09-938-842A-694 US-10-108-26A-1417 US-10-28-1 US-10-027-632-77120 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121 US-10-027-632-77121	0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632- 0.027-632-	US-10-398-221-684 US-10-114-170-240 US-10-412-277-3 US-10-398-221-10 US-10-398-221-2058 US-10-081-051-61
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Sequence 30, Application US/10313994

Publication No. US20030162718A1

GENERAL INFORMATION:

APPLICANT: Tang, Yi-Quan

APPLICANT: Yuan, Jun

APPLICANT: Vuan, Jun

APPLICANT: Which and Michael E.

TILE REFERENCE: P-UC 3095

CURRENT APPLICANTON NUMBER: US/10/313,994

CURRENT APPLICATION NUMBER: US/10/313,994

PRIOR FILING DATE: 1999-05-10

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGACCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-313-994-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 132; DB 15; Best Local Similarity 100.0%; Pred. No. 7.8e-41; Matches 132; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
US-10-313-994-30
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77713
LENGTH: 450
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1 Similarity 52.8%;
66; Conservative (
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Best Local Similarity
Matches 66; Conserv
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                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-77713
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ORGANISM: Human
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Matches 6
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                                                                                                                                                                   Sequence 31, Application US/10313994

Publication No. US20030162718A1

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: PUC 3095

CURRENT FILING DATE: 2002-12-05

CURRENT FILING DATE: 2002-12-05

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 31

LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGTGAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAAC 120
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| Bublication No. US20020198371A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: POLYMORER: US/10/027,632
| CURRENT APPLICATION NUMBER: US 60/218,006
| PRIOR APPLICATION NUMBER: US 60/18,006
| PRIOR FILING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 1999-04-20
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-09-28
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Best Local Similarity 90.0%; Pred. No. 5.5e-32;
Matches 117; Conservative 0; Mismatches 13; Indels 0;
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ORGANISM: Artificial Sequence
                                                           121 AATATTACAGTG 132
                              121 AATATTACAGTG 132
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Sequence 77713, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION: Polymorphisms in the Human Genome

PRICR PELING DATE: 2000-04-20

PRICR PELING DATE: 2000-04-20

PRICR PELING DATE: 2000-04-20

PRICR PELING DATE: 2000-04-20

PRICR PELING DATE: 2000-03-24

PRICR PELING DATE: 1999-11-23

PRICR PILING DATE: 1999-11-23

PRICR PILING DATE: 1999-11-23

PRICR PILING DATE: 1999-10-24

PRICR PILING DATE: 1999-10-24

PRICR PILING DATE: 1999-09-08-09

PRICR PILING DATE: 1999-09-08-09

PRICR PILING DATE: 1399-09-08-09

NUMBER: OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SETURN APPLICATION NOT713
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                                                                                                                                                                                                                                                                                              64 GADAGICTCAGTTTCCGAACTCCACGTADACGTGTGCTCCTAAGACGGCADACAAT
                                                                                                                                                4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGGAGGT
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23.2%; Score 30.6; DB 13; Length 450; 52.8%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30.6; DB 16; Length 450; Pred. No. 0.27;
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PRIOR APPLICATION NUMBER: 60/048,880
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR PRIOR APPLICATION NUMBER: 60/048,896
PRIOR PRIOR OFFIEL 1997-06-06
PRIOR PRIOR DATE: 1997-06-06
PRIOR PRIOR DA
         1997-06-06
                                                                                                                                      Sequence 4727, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AECONICA.~2.
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: MAP TO AB022537.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BALLA : SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BTALL LIVER, SIGNAL = 3.5

OTHER INFORMATION: EST_HUMAN HIT: BG680371.1, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: Of1187, EVALUE 9.60e-01

OTHER INFORMATION: LST_HUMAN HIT: BG680371.1, EVALUE 0.00e+00

US-10-029-386-4727
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Publication No. US20030181692A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TILLE OF INVENTION: 207 Human Secreted Proteins

FILLE REFERENCE: P2007P2

CURRENT APPLICATION NUMBER: US/09/933,767

CURRENT PILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: OF/1801/05614

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1908-12-04

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-06-04

PRIOR FILING DATE: 1998-06-06

PRIOR APPLICATION NUMBER: 60/049,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                                                                                       SULT 5
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/068,064
FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/068,054
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                                                                                                                                                                                       Gaps
                                                                                                                                                                                    ;
0
                                                                                                       Score 30.6; DB 13; Length 1985;
Pred. No. 0.46;
0; Mismatches 59; Indels 0;
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TITLE OF INVENTION: 207 Human Secreted Proteins
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
EARLIER PILING DATE: 1998-06-04
EARLIER PILING DATE: 1998-06-04
EARLIER PILING DATE: 1998-06-04
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE:
, OTHER INFORMATION: n equals a,t,g, or c US-10-004-860-97
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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                                                                                                               Query Match 23.2%;
Best Local Similarity 52.8%;
Matches 66; Conservative
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; Sequence 97, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TILE REFERENCE: PZ007P1
; CURRENT RELIGN NUMBER: US/10/004,860
; CURRENT FILION NUMBER: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30.6; DB Pred. No. 0.46; 0; Mismatches
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US-09-933-767-97
       PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR PELLING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-05-18
PRIOR PLING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-15
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Query Match 23.2%; Best Local Similarity 52.8%; Matches 66; Conservative

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RESULT 7 US-10-004-860-97

TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: SITE

SOFTWARE: Patentin Ver. 2. SEQ ID NO 97 LENGTH: 1985

TYPE: DNA ORGANISM: Homo sapiens

FEATURE:

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4 ccrrcrrracragraccarraccaagraangaaarrgraccegacrrrrgccegcgagaager 63
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23.2%; Score 30.6; DB 16; Length 1987;
Best Local Similarity 52.8%; Pred. No. 0.46;
Matches 66; Conservative 0; Mismatches 59; Indels 0;
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERRNCE: PA11P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-19
PRIOR PILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 115
LENGTH: 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (5). (5) OTHER INFORMATION: n equals a,t,g, or c
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                                                     EARLIER APPLICATION UNDER: 60/048,970
EARLIER PILING DATE: 1997-66-06
EARLIER FILING DATE: 1997-66-06
EARLIER FILING DATE: 1997-66-06
EARLIER FILING DATE: 1997-66-06
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EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER PAPLICATION NUMBER: 60/048, 963
EARLIER PAPLICATION NUMBER: 60/048, 963
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER PILING DATE: 1998-07-15

SEQ ID NO 97

LENGTH H. 1985
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LOCATION: (332)
OTHER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
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Sequence 34481, Application US/10369493

Sequence 3481, Application US/20305357541

Sequence 3481, Application US/20305357541

Sequence 3481, Application US/20305357541

Sequence 3481, Application US/20305357541

Sequence 3481, Application US/20396493

APPLICANT: Glodman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF TITLE OF INVENTION: UNMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374

SEQ ID NO 33481
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Best Local Similarity 56.61
Matches 56; Conservative
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1583 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTCCAAAATGGCCTTTATC 1642

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RESULT 9
US-10-264-237-115
US-10-264-237-115

, Sequence 115, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:

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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 60/198,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-33
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-11-30
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                                                       Gaps
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Sequence 1786, Application US/10087192

Sequence 1786, Application US/10087192

PUBLication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: CANCER

TITLE OF
                                                       27; Indels
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Best Local Similarity 62.0%; Pred. No. 7.5; Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38125, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3568 Trcrrcaccaa 3558
                                                                                                                                                                                                                                                                                                                                                                                                                 108 TAAGACGGCAA 118
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 56; Conserv
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| Sequence 37892, Application US/10437963
| Publication No. US20040123343A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J. APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| APPLICANT: Wu Wei
| APPLICANT: White Marey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li Ping N. Nucleic Acid Molecules and Other Molecules Associated With TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B CURRENT APPLICANTON NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 SEQ ID NOS: 204966 | SEQ ID
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CURRENT PILING DATE:
CURRENT PILING DATE:
APPLICANTON NUMBER: US 60/214,087
PRIOR PILING DATE:
PRIOR PILING DATE:
APPLICANTON NUMBER:
BRIOR FILING DATE:
APPLICANTON NUMBER:
BRIOR FILING DATE:
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Pred. No. 5.6;
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                                                                                                                                                                                                                                    Sequence 863, Application US/09887576
Patent No. US20020144047a1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
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Best Local Similarity 55.8%;
Matches 53; Conservative (
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ORGANISM: Oryza sativa
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US-10-027-612-38125/c

Sequence 38125, Application US/10027632

Bublication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: O-1/Ymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/18,006

PRIOR APPLICATION NUMBER: US 60/19,636

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-08

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FEATURE FEATURE WINDOW VERSION 4.0

SEQ ID NO 38125

LENGTH: 409
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20.3%; Score 26.8; DB 13; Length 409;
Best Local Similarity 55.3%; Pred. No. 7.8;
Matches 52; Conservative 0; Mismatches 42; Indels 0.
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SCFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38125
LENGTH: 409
TYPE: DNA
ORGANISM: Human
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; ORGANISM: Human
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Search completed: October 11, 2004, 12:14:32 Job time : 217 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

October 11, 2004, 08:56:11 ; Search time 1398.5 Seconds (without alignments) 2818.597 Million cell updates/sec US-10-009-317A-30 132 1 ggaccttgtctactagtccc......cggcaaacaatattacagtg 132 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Run on:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ę	BX3384	RC1-H	BONBK	Drosor
Description	BX338407 BX338407	BF088574 RC1-HT088	BZ475082 BONBK72TF	A1.105776
	BX338407	BF088574	679 28 BZ475082	CNS0150E
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% Query Match Length DB	1201	193	619	1007
% Query Match	24.4	23.3	23.3	23.3
Score		30.8	30.8	30.8
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2058 RC3-GN02 2068 RC3-GN02 2060 RC3-GN02 7927 QV0-DT00 281 wk90f12.x 405 nn57h03.8	29619 29619 5016 2018 3092 74818	97439 hr80f02 30065 ij84b01 7084 wp72h04. 72572 ig99g05 53090 6030259	3219 AU148 36052 UI-H 4596 AU154 51661 OI-5 51661 UI-5 51061 UI-5 51001 ik90 76480 6014	3376 UI.H-PL 5400 XX79503 6400 XX.9503 738 WOLDDD. 6431 UI.H-PFH 6417 UI.H-PEK 6177 UI.H-PEK 6177 UI.H-PEK 7608 UI.H-PFL 7608 UI.H-PFL 7617 GOZG292 8127 ALSS2828
20 12 BI05206 48 12 BI05206 65 12 BI05206 02 10 AW93792 31 9 AAB97781 51 9 AA\$976 53 10 AW43976	60 \ 10 AW2478 67 10 AW1296 67 10 AW1501 68 10 BE2201 77 9 AI39309 89 10 AW67108 90 9 AW07108	94 10 BF1974 06 13 BQ1300 09 9 A193708 10 12 BM2725 19 12 B17530 42 14 CA8660	65 9 AU14821 66 12 BO0060 67 12 BO060 70 9 AA15604 75 12 BM6716 75 12 BG3250 19 10 BE8764 19 12 BI0919	35 14 CA42337 39 10 AW474307 14 12 BW474307 31 9 AI922738 38 13 BUG1831 42 14 CB25048 51 13 BQ55617 51 14 BQ5617 51 14 BQ56037 52 12 BQ68037 53 AIS2282
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases: 1 to 13)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Carolho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Gollveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Fax: +55-11-2707001
Email: asingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCl-HT0881-130
900-014-bl1&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence start: 28
High quality sequence story: 192. BF088574 130900-014-bll HT0881 Homo sapiens cDNA, mRNA sequence. BF088574 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Shotgun sequencing of the human transcriptome with ORF expressed roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) el: +55-11-2704922 RESULT 2 BF088574/c DEFINITION ACCESSION SOURCE ORGANISM MEDLINE PUBMED REFERENCE AUTHORS VERSION KEYWORDS JOURNAL FEATURES TITLE COMMENT LOCUS

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/db_xrefe="taxon:9606"
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/clone_lib="HT081"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_2: Smal;
/note="Organ: head_note: head_n ö 62 22 111 Accreaetecresecreariaersarseaserarecreerraaeaareresere 3 ACCTIGICIACIAGICCCTIACCGAGIAAGGAAAIGIACCGGACITIIGCGGCGAGAAGG Gaps ö 23.3%; Score 30.8; DB 10; Length 193; 55.7%; Pred. No. 8.3; 108 51 recaachterecitéchierearreitentraakteageareit 6 Indels 63 TGAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCT 47; 0; Mismatches mol_type="mRNA" Conservative Similarity 59; Query Match Best Local Matches

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Gaps

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63

679 bp DNA linear GSS 13-DEC-2002 BONBX72TF BO 1.6 2 KB tot Brassica oleracea genomic clone BONBK72, genomic survey sequence. Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BONBK72TR BZ475082.1 GI:26776627 TIGR DEFINITION SOURCE ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS JOURNAL COMMENT RESULT 3 BZ475082 TITLE

Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Staprimer: TF Class: sheared ends. 9712 Medical Center Drive, Rockville, MD 20850, Location/Qualifiers Tel: 301-838-3523 Fax: 301-838-0208 6. .679 FEATURES

/clone lib="BO_1.6 2 KB tot" /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers" 0 Length 679; 47; Indels DB 28; /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="Tol00DH3" /db_xref="taxon:3712" /clone="BONBK72" Score 30.8; Di Pred. No. 13; 0; Mismatches 23.3%; Conservative Similarity 59; Query Match Best Local Si Matches 59,

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/organism="Homo sapiens"

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Gaps

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Shotgun sequencing of the human transcriptome with ORF expressed
                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
  O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.,
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                                                                                                                                 CNSO15QE 1007 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN14804 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL105776.1 GI:5618284
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhin; Hominidae; Homo.

(bases 1 to 320)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
                                                                                                                                                                                                                                                                                                                                                                                         Genoscope.

Birect Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a ttp://www.edgp.ebi.ac.uk - This Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEBH (Centre du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="raxon:7227"
/clone="BACN14B04"
/clone=lib="DrosBAC"
/plasmid="pBeloBAC11"
/note==end : T7"
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34.8%; Pred. No. 15;
ive 30; Mismatches
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Drosophila melanogaster
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/unl_type="maxx" saptement / unlight / unlight
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Fax: +55-11-270001
Email: asimpson@ludwig.org.br
Pris sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-h08&t2=2001-01-7xt4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence start: 6
High quality sequence stop: 320.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (Bases I to 348)

1 bosses. Ito 348)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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    .320
    /organism="Homo sapiens"

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Homo sapiens
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de Souza, S.J. and

TITLE

COMMENT

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (Dases I to 402)

1 blases I to 402)

1 blases I to 402)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Burnstein, A., deoll'veira, F.S., Bucher, P., Jongeneel, C.V., O'Harce, M.J., Soares, F.F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Paroject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-a07&t3=2001-01-17&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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QV0-DT0047-170200-122-h12 DT0047 Homo sapiens CDNA,
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52.8%; Pred. No. 12;
cive 0; Mismatches
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/organism="Homo sapiens"
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High quality sequence start: 51
High quality sequence stop: 365.
                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                     Contact: Simpson A.J.G
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                                                                                                                                                                                                                                                                rel: +55-11-2704922
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases I to 365)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneal, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL futp://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-GN0268-170101-012-d008£3=2001-01-17&t4=1)
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RC3-GN0268-170101-012-a07 GN0268 Homo sapiens CDNA, mRNA sequence.
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/clone_lib="GN0268"
/clone_lob="GN0268"
/clone_lob="GN0268"
/note="Grgan: placenta_normal; Vector: puc18; Site_l:
Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Shocgun sequencing of the human transcriptome with ORF expressed
sequence tags
             Shotgun sequencing of the human transcriptome with ORF expressed
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                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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; Pred. No. 12;
0; Mismatches
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High quality sequence stop: 348.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI052060.1 GI:14459590
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52.8%;
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E 1 (bases 1 to 4)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapberfamil.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-DT0047-170
200-122-hlz&t2=2000-02-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 402.
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                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 13;
0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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/dev_stage="adult"
/lab_host="nulus" (phage-resistant)"
/clone_lib="NCI CGAP_Luly"
/clone_lib="NCI CGAP_Luly"
/note="forgan: lung; Vector: pt7730-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Scares and M. Fatima Bonaldo. "
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nn57h03.81 NCI_CGAP_Kid6 Homo sapiens cDNA clone IWAGE:1088021 3',
AAS93405
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Email: cgapbs.remail.ihh.gov

Email: cgapbs.remail.ihh.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thmor Gene Index
Unpublished (1997)
                                                                                                                                                                                                1. 431
/organism="Homo sapiens"
/mol_ype="mRNA"
/db xref="texton:9606"
/clone="IMAGE:2422703"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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   Clone distribution: NCI-CGAP clone distribution information
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                        found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 916 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 413.
Location/Qualifiers
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63

Gaps ö

ORIGIN

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Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project (Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LuNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross match from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more I residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2820449.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820449 3', AW247815
               /clone lib="NCI_CGAP_Ut2"
/note="Organ: uterus; Vector: pCNV-SPORT6; Site_1: Sall;
/note="Organ: uterus; Vector: pCNV-SPORT6; Site_1: Sall;
site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                 436 ccrircacircccaecacciriecccaacaeaaraaecresarccccrireecerrereaarar 377
                                                                                                                                                                                                                                                                                                                             64 GAAAGTCTCAGGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                                                                                                                                                376 CCCAGIGICITICAGGIIIICCCAAGACCACTICCCTGIGGCCTICCAAAATGGCCTTTAIC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (Dases 1 to 460)
NH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Other ESTs: 2820449.Sprime
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cione="INAGE:2820449"
/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab host="MH10B (phage-resistant)"
/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
Scots: cDNA made by oliqo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'
                                                                                                                                                                                                                                            4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                                                                                                               Length 453;
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                                                                                                                                                             DB 10;
                                                                                                                                                                                                       59;
                                                                                                                                                             23.2%; Score 30.6; D
52.8%; Pred. No. 13;
:ive 0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence stop: 326.
Location/Qualifiers
'lab_host="DH10B"
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  124 ATTAC 128
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                                                                                                                                                                    Query Match
                                                                                                                                                                                            Local
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AW247815/c
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 23.2%; Score 30.6; Dilarity 52.8%; Pred. No. 13; Conservative 0; Mismatches
                                                                                     /organism="Homo sapiens"
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                                                                                                      mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1088021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW439761.1 GI:6975067
                                                                                                                                                                        /sex="mixed"
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Best Local Similarity
Matches 66; Conserv
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AW439761/c
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AW129619

467 bp mRNA linear EST 25-OCT-1999

AND ARABAN STATE CARP_Ut4 Homo sapiens cDNA clone IMAGE:2607615 3',
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//note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
                                                                                                                                                                                                                                          64 GAAAGICTCAGICGCITICCGAACTCCAGIDAAACGIGGCCTCCIAAGACGGCAAACAT 123
380 CCCAGIGICTICAGGIIICCAAGACCACTICCCTGIGGGCTTCCAAAIGGCCTTTAIC 321
                                                                                                                                                                                                            440 cérricacircedededécrirececaacadaraagerigaarececriredecrrendaarar 381
                                                                                                                                                                               63
adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:2607615"
/tissue_type="serous papillary carcinoma, high grade,
                                                                                                                                                                            4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                                                                                              Gaps
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0
                                                                                                               Length 460;
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Best Local Similarity 52.8%; Pred. No. 13;
Matches 66; Conservative 0; Mismatches 59;
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Best Local Similarity 52.8%; Pred. No. 13;
Matches 66; Conservative 0; Mismatches
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EST.
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Homo sapiens
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AW129619
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AW129619/c
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Indels

Length 467;

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: gagpbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: gagpbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 416.
                                                                                                                                                                                                                                                                                                                                                                   AWISO166 467 bp mRNA linear EST 03-NOV-1999
3436604.x1 NCI_CGAP_Utl Homo saplens CDNA clone IMAGE;2629638 3',
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adenocarcinoma, 7 pooled tumors"
| Jab host="DH108"
| /clone lib="NLI CAAP Utl"
| /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
| Sale_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
| Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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                          435 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGCTTTTGAATAT 376
                                                                                                                                        375 cccadigicircadoririccaladaccacricccrolidaderrecaladadadecrirare 316
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                                                                                                64 GAAAGTCTCAGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
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63
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CCTTGTCTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 467
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2629638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW150166.1 GI:6198051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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Best Local Simil
Matches 66; (
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AW150166/c
LOCUS
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Tunor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Preparation: M. Bento Scares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lb="NCI CGAP_Lu24"
/note="Organ: lung; Vector: pT7F3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP_LuS was prepared, and ss circles were made in vir.o. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 144920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                               BE220183 468 bp mRNA linear EST 03-JUL-2000 hv69b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178651 3',
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BE220183.1 GI:8907501
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                                                                                                                 mRNA sequence.
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AUTHORS
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Search completed: October 11, 2004, 10:55:04 Job time: 1403.5 secs

Run on:

October 11, 2004, 08:25:36; Search time 1124.5 Seconds (without alignments) 5087.844 Million cell updates/sec 1 ggacctcgtctactagtccc......cggttgacaatatttccgca 132 6940544 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 Gensmbl:*

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18: 9D pat:* US-10-009-317A-31 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Scoring table: Database : Sequence: Searched:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AL844144 178965 bp DNA linear ROD 16-MAY-2003 Mouse DNA sequence from clone RP23-204D17 on chromosome 2, complete sequence.
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Antimicrobial theta defensins and methods of using same
Patent: WO 0068265-A.3 ol.6-NOV-2000;
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0; Mismatches 13; Indels
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Matches 117; Conservative 0; Mismatches 13;
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/noTe="Synthetic Construct"
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Patent: WO 0068265-A 31 16.NOV-2000;
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live 0; Mismatches 0;
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Construct"
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-55K6
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made too resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSROCT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at from the Rec1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Sequence version replaced gi:30140518. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a prized quality of at least 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC107644 241189 bp DNA linear HTG 02-MAY-2003 Mus musculus clone RP23-55K6, *** SEQUENCING IN PROGRESS ***, 14 ordered pieces.
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                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117188 rcrcaccacrcaacdaaccraaccaactarcrd 117154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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1. .178965
                              Mus musculus (house mouse)
                                                                                                                                                        (bases 1 to 178965)
                                                                                                                                                                                          Almeida, J.
Direct Submission
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AC107644/c
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FEATURES

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Signature, S. (Dascal Lt o 24118).

Bitten, B. (Lincoll., Nusbbaum,C., Lander,E., Ali,A., Allen,N., Andersa, J. (Dangolano, A., Changolano, A., Cooke, P., Dardolano, K., Dewar K., Diaz,J.S., Dodge,S., Parc,S., Cooke,P., Dardolano, K., Dewar K., Diaz,J.S., Dodge,S., Parc,S., Gooke,P., Dardolano, K., Dewar K., Diaz,J.S., Dodge,S., Parc,S., Gande,S., Gooke,P., Dardolano, K., Dangolano, J., Grand-Pierre,N., Hagoo,B., Horton,L., Hulme, W., Illey, I., Ohnson, R., Jones,C., McCarthy,M., McChang, A., Karatas,A., Kalles,C., LaRocque,K., Lamazares,N., Manchas,A., Kalles,C., LaRocque,K., Lomazares,N., McDang, T., Choncall,P., Deltare, N., McDang, Y., Margor, J., Marquis,N., Matthews,C., McCarthy,M., McDang, Y., Margor, J., Marquis,N., Matthews,C., McCarthy,M., McDang, Y., Margor, J., Marquis,N., Peters,R., Riebeck,M., Schlano, J., Nebana, S., Schupbeck,R., Seman,S., Severy,P., Spencer, B., Stancos,R., Schupbeck,R., Schupber,R., Schupbe
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 241189)
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Chaese 1 to 5339)

Okazaki, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.

Direct Submitssion

Submitted (23-701-2003) Hisashi Koga, Kazusa DNA Research

Institute, Laboratory for Genome Informatics; 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

The CREATE program supported by Japan science and technology

corporation; cDNA full insert sequencing: Kazusa DNA Research

Institute; cDNA library construction, clone selection and 5'- &

Location/Qualifiers
Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <258. .2834
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is not identified."</pre>
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PRANASRFISAEAGRYVYSAPIRROLASRGSSICHVDVSDKADDDVDLEGISWDAPGY
ROGDVULSKNIRSDDITSGYYTDGGLGLYTRRLNRLPDGMAVVRETLQRNTSLGLGDA
DR."
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VEMQSSASSKDSSQSKIIRFTLGQKKISRLPQPTARVAAAGSEAKTRGGSAAANNRRS
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EKLKLFNSKGGSKAGEGSASRDTSCERLEIILPSFEETEELEATANRALSTVGPASSSP
KIALKGIAQRTFSRALTNKKSSPKGNEKEKEKOQQREKEKEKEKEKKKDITKRVSVTDR
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AESSSAGVSMEPSHYTKSGQPALEELTEDPEARRLRTVKNIADLRQNLEETMSSLRGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
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55.8%; Pred. No. 35;
iive 0; Mismatches

    .5339
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                                                                                                        DNA Res. 10 (4), 167-180 (2003)
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Matches
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AC120854
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       TITLE
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Saga,Y., Nagase,T., Ohara,O. and Koga,H.
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Mus musculus
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                         This sequence will be replaced

* Dy the finished sequence as soon as it is available and
the accession number will be preserved.

* 2836 2835: Gap of 100 bp

* 2836 28373: Gap of 100 bp

* 28474 28148: contig of 2675 bp in length

* 2849 44862: Gap of 100 bp

* 44863 44962: gap of 100 bp

* 44863 4959: contig of 1614 bp in length

* 4966 50059: gap of 100 bp

* 6966 60823: contig of 10764 bp in length

* 6966 60823: contig of 10764 bp in length

* 60824 60923: gap of 100 bp
                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.7%; Score 32.6; DB 2; Length 241189;
.larity 58.9%; Pred. No. 9.3;
Conservative 0; Mismatches 39; Indels 0;
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9: contig of 26261 bp in length
9: gap of 100 bp
1: contig of 3568 bp in length
9: gap of 100 bp
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    .241189
    /organism="Mus musculus'

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DEFINITION

LOCUS

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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Gaps

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note="assembly_fragment"
08838. 142158
'note="assembly_fragment"
Center clone name: 329 B 6
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                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 207736)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                        Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-329B6 Unpublished
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                                                                HTG: HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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AC120854.3
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COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 204630 bases at least Q40 Consensus quality: 205639 bases at least Q30 Consensus quality: 205631 bases at least Q30 Insert size: 199000; agarose-fp Insert size: 206636; sum-of-contigs Quality coverage: 8.2 in Q20 bases; sum-of-contigs Quality coverage: 7.9 in Q20 bases; sum-of-contigs
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Allen H., Adyagi, A., Aydej, M., Baca, E., Baden, H.,

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                            ch 23.0%; Score 30.4; DB 2; Length 20 1 Similarity 55.8%; Pred. No. 52; 58; Conservative 0; Mismatches 46; Indels
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Rattus norvegicus (Norway rat)
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AL SUDMITTEE SUDMITTEE (08-COT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21671637.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a 'working draft' sequence. It currently consists of 3 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                            Vorley, K.C.

Vorley, K.C.

Direct Submission

Direct Submission

Direct Submission

Submitted (129-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Dases 1 to 216422)

Rat Genome Sequencing Consortium.

Direct Submission
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Contact: hgsc-help@bcm.tmc.edu
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Web site: http://www-seq.wi.mit.edu
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Center clone name: 73_B_
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                                                                                                                                                                                                                                                                                                                                        ROD 30-SEP-2003
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Birren, B., Nusbaum, C. and Lander, B.

Mus musculus chromosome 7, clone RP23-73B20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC119848 239297 bp DNA linear ROD 30-SEP-:
Mus musculus chromosome 7, clone RP23-73B20, complete sequence.
                                                                                                                                                                                                                                                                           32 GGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAAGTCTCAGTCGCTCTCCGAACTCCA
                                                                                                                   Match 23.0%; Score 30.4; DB 2; Length 216422; Local Similarity 59.1%; Pred. No. 52; Conservative 0; Mismatches 36: Indels n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109248 cagradagachcchacachaccachran 109275
                                                                                                                                                                                                                                                                                                                                                                                                             92 CGGAAACGTCTGCTCCTCAAACGGTTGA 119
211584. .213497
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AC119848.8 GI:33438673
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   misc_feature
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TITLE
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AUTHORS
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AUTHORS
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Direct Submission

Direct Submission

Burnitted (165-Aug-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Es (basea 1 to 23929)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camaraca, J., Chang, J., Choepel, Y., Cock, A., Cock, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, E., Hados, E., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Uncaras, A., Kells, C., Landers, T., Levine, R., Machan, J., Mand, J., Matchews, C., McCarthy, M., Mador, J., Mador, J., Matchews, C., McCarthy, M., Micol, R., Micol, R., Mahor, J., Mahon, J., Cohonnell, P., Naylor, C., Nicol, R., Mahor, J., Mensama, V., Cohonnell, P., Radman, J., Schubs, M., Talamas, J., Tesfaye, S., Theodor, J., Topham, S., Severy, P., Smith, C., Nassillev, H., Venkataraman, W. S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassillev, H., Venkataraman, J., Zembek, L., Zimmer, A. and Zody, M., Allen, S., Nasie, S., Shubs, M., Marther, S., Mand, M., Wassillev, H., Venkataraman, W. S., Viel, R., Wo, A., Wilson, B., Mand, M., Mand, M., Mand, M., Mand, M., M., Mand, M., M., Mand, M., M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., M., Mand, M., Direct Submission

Submitted (18-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (basea 1 to 233237)

Birren, B., Wusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Cheepel, Y., Colymore, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Gadagan, J., Garad, Pierre, N., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kalls, C., Landers, T., Levine, R., Maccon, J., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Micol, R., Norbu, C., O'Connor T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauper, R., Seaman, S., Schupback, R., Seaman, S., Schupback, R., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vornig, G., Zahnoun, J., Zahmer, A. and Zody, M. Direct Sumfission. Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teglage, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkaraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Submitted (30-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 5, 2003 this sequence version replaced gi:32964951. ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Contact: sequence_submissions@genome.wi.mit.edu ω

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                                                                                        misc_feature
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Direct Submission

Submitted (104-ARR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

numguery@sanger.ac.uk Clone requests in: 6941163.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone, as we submit sequences with

oorresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subbclone or more than one Mil subclone; and the assembly was contirred by resolved primary accession numbers given in the feature table with their source databases: Em: FRBME, Sw: SWISSPROT; Tr:, TREMBE, Wp:, WORVEPP: Information on the WORWEPP database can be found in the advanced and the database can be found and the database can
                                                                                                                                                                                              AL589766 176183 bp DNA linear ROD 05-APR-2002
Mouse DNA sequence from clone RP23-19G4 on chromosome 13, complete
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                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-19G4 is
from the RPCI-23 Mouse PAC Library
                                                                                                                                      15 AGTCCCTTACCGAGTAAGGAAATGTGCCCGACTTTTGCGGCGAAAGGCCGAAAGTCTCAG
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For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
Location/Qualifiers
Length 239297;
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       DB 10;
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   23.0%; Score 30.4; D
55.8%; Pred. No. 53;
live 0; Mismatches
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                                                                      Conservative
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8 Birren, B. Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barra, M., Bastien, V., Bloom, T., Boguelavity, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., District, B., Dodge, S., Cooke, P., DeArellano, K., Dewar, K., District, B., Dodge, S., Cooke, P., DeArellano, M., Gage, D., Galagan, J., Garder, S., Gorder, G., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Lite, J., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Mandonald, P., Major, J., Matthews, C., Kartasa, A., Kells, C., Landers, T., Maloga, V., Murphy, T., Naylor, J., Naylor, J., Matthews, C., Micol, R., Narbu, C., Norman, C., Ponnen, D., Patere, N., Raymond, C., Nachl, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Nachl, D., Oliver, J., Peterson, K., Ponnen, J., Roman, J., Roy, A., Saylor, J., Raymond, C., Rette, R., Rise, G., Gevery, P., Smith, C., Spencer, B., Stanger-Thoman, N., Stojanovic, N., Talamas, J., Teffaye, S., Theddore, J., Tophan, K., Travers, M., Vassiliev, H., Viel, K., Wilson, B., Stanger-Thoman, M., Allen, M., Viel, K., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Burna, J., 20 Charles Street, Cambridge, MA 02141, USA

Seearch, 320 Charles Street, Cambridge, MA 02141, USA

Seearch, 320 Charles Street, Cambridge, MA 02141, USA

Seearch, J.S. Dodge, S., Dooley, W., Bastien, V., Bloom, T., Collymore, A., Cook, A., Wilson, M., Hafez, N., Gardyna, S., Gollymore, A., Cook, A., Walser, B., Mabalum, C., Lander, B., Mabbit, R., Marsaham, C., Hagos, B., Hall, M., Barna, M., Hafez, N., Machalano, K., Hados, M., Marsaham, C., Stodes, S., Dodge, B., Golds, M., Hagos, M., Hagos, B., Hall, M., Madonald, P., Major, U., Manning, J., Matcha, M., Wassila, M., Wasaila, M., Wanasa, J., Peterson, K., Phukhan, P., Woung, G., Schauer, S., Thecdor, T., Pohnson, R., Retta, R., Ramasan, J., Peterson, K., Phuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19480?)
Birrar, B., Vusbaum, C. and Lander, E.
Mus musculus chromosome 1, clone RP23-249L15
Unpublished
41372 TAGTTATCTGTCACTGAATAAGGAATTATACCAGATTTTAGCAGCATCATGCAGAAACAC 41431
                                                                                                                                                                                                                                                                                                                      AC129542 194807 bp DNA linear ROD 26-SEP-2003
Mus musculus chromosome 1, clone RP23-249L15, complete sequence.
AC129542
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4 (Dases 1 to 194807)
Direct Submitted (13-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                               41432 TTAGTATCTCTACCAGTCTTAAATTTC 41462
                                                                           71 TCAGTCGCTCTCCGAACTCCACGGAAACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL; Sww., SWISSEROT; Tr., TREMBL; Wp., WORNPEP; Information the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-278P12 is from the MORNPEP database BAC Library proposity the group of Pieter de Jong.

FOR further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 17, 2003 this sequence Version replaced 9:30350055.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                                                                                                                                                                                      BX248984 191884 bp DNA linear ROD 17-JUN-2003 Mouse DNA sequence from clone RP23-278P12 on chromosome 1, complete
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Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                       76234 AGAATTACACAGAACTTGGAGATTTTTAAAC 76264
       83 CGAACTCCACGGAAACGTCTGCTCCTCAAAC 113
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/mol_type="genomic DNA"
/db xref="taxon:10090"
/chromosome="1"
/clone="RP23-278P12"
/clone="lb="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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1. .191884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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ORIGIN

FEATURES

'rpt_family="L1_MM"

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                     Birren, B. Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Cocke, P., Corum, B., DeArellano, K., Collymore, A., Cocke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferrelara, P., Firederald, M., Gaga, D., Galagan, J., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamaft, A., Kartacas, A., Kalls, C., Landers, F., Machen, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mabbitt, R., Machen, C., McCarthy, M., Manning, J., Manning, J., Mushang, P., Pierre, N., Norol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petroson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vola, K., Viel, R., Vola, R., Vola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 2003 this sequence version replaced gi:32328999. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
_------ Project Information
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clone_lib="RPCI-23 Female Mouse BAC"
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complement(6491..5788)
/rpt_family="Lx5"
6490..6679
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/db_xref="taxon:10090"
/chromosome="1"
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rpt_family="Lx"
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Center clone name: 249_L15
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clone_end:SP6
site:EcoRI"
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/rpt_family="L1_MM"
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rpt_family="Lx2"
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124982 TAGTTATCTGTCACTGAATAAGGAATTATACCAGATTTTAGCAGCATCATGCAGAAACAC 125041
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omplement(10279. .10540)
rpt_family="Lx5"
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complement(12336. .13145)
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complement(8695. .8850)
/rpt_family="MT2B"
complement(8861. .9036)
/rpt_family="L1_MM"
/rpt_family="URR1A"
complement(8163, .8222)
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ement(9027
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                             complement(8163. .8222)
'rpt_family="CYRA11_MM"
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/rpt_family="MT2C"
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8658. .8678
/rpt_family="AT_rich"
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8461. .8630
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16191..16218
/rpt_family="AT_rich"
17488..17665
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25756. .26039
/rpt_family="Lx9"
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0908. .11085
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family="AT_rich"
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0820. .10862
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. .11222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt family="L1VL2"
.5632. .16189
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22199. .22303
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                                                                                                                                                                                                                                                                                                                          "LX5"
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4137. .14260
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:0986. .21988
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2409.
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All Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON Sep 19, 2002 this sequence version replaced gi:21747328
The sequence in this sasembly is a combination of BAC based reads and whole genome shotgun sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center: Center College of Medicine
Center clone and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Daylor College of Medicine
Center clone name: CH230-457M16

Consensus quality: 155192 bases at least Q20
Consensus quality: 155192 bases at least Q20
Consensus quality: 155122 bases at least Q20
Estimated insert size: 175472; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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Molecular and Human Genetics, Baylor College of Medicine, One /lor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
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/note="wgs_contig"
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Ruzny, D.Marie, Marzker, M.Lee, Abramzon, S., Adams, C., Alder, J., Angland, D. Marie, M. Carzker, M.Lee, Abramzon, S., Anin, A., Anguinano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bader, H., Bandhmed, F., Balden, L., Bandarmaike, D., Barber M., Barastead, M., Benahmed, F., Biswalo, K., Bandarmaike, D., Barber M., Barastead, M., Benahmed, F., Biswalo, K., Barder, M., Breach, D., Borzan, C., Caver, C., Caver, C., Chen, J., Chen, J., Chu, J., Cheveland, C., Cockell, R., Carter, M., Carter, C., Coyel, M., Cree, J., Border, D., Dandon, C., Coyel, M., Cree, D., Dandon, C., Carter, M., Martin, M., Martin,
                                                                                                                                 193304 bp DNA linear HTG 19-SEP-2002
Rattus norvegicus clone CH230-457M16, *** SEQUENCING IN PROGRESS
AC118868
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Direct Submission
Submitted (21-APR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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      125042 TTAGTATCTCTATCCAGTCTTAAATTTC 125072
                                                                                                                                                                                                                                                                                              AC118868.3 GI:23194649
HTG; HTGS PHASE1; HTGS DRAFT; F
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Nazay, Dasses 1 to 239140)

Rallen, C. Allen, H. Alsbrooks, S. Amin, A. Agguano, D.

Anyalebechi, V. Avorgi, A. A. Agguano, D.

Anyalebechi, V. Angerike, D. Barber, W. Barnstead, Benahmed, F.,

Biswalo, K. Blair, J. Blankenburg, K. Blyth, P. Brown, M.

Biswalo, K. Blair, J. Blankenburg, K. Blyth, P. Brown, B.

Cardenas, V. Carter, C. Caraczos, I. Casar, H. Center, A.

Cardenas, V. Carter, K. Caraczos, I. Casar, H. Center, D.

Cardenas, V. Carter, C. Chen, G. Chen, Y. Chen, Z. Chen, Z.
                           ALUMYZYB 239140 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-40116, WORKING DRAFT SEQUENCE, 5
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3 (bases 1 to 239140)
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                        DRAFT; HTGS_FULLTOP
                                                                                                                                                                                      AC099298.7 GI:30580785
HTG; HTGS_PHASE1; HTGS_DRAFT; PRattus norvegicus (Norway rat)
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Direct Submission
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Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (13-WAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:25085778.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence ontigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: CR30-40116
Assembly program: Atlas 3.0;
Consensus quality: 225133 bases at least Q40
Consensus quality: 227827 bases at least Q30
Consensus quality: 230020 bases at least Q30
Estimated insert size: 239353; aum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the fainshed sequence as soon as it is available and the accession number will be preserved.
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64407: gap of unknown length
223476: contig of 159069 bp in length
223576: gap of unknown length
227284: contig of 3708 bp in length
227384: gap of unknown length
31763: contig of 4379 bp in length
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4 239140: contig of 7277 bp in length.
Location/Qualifiers
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                     AUTHORS
TITLE
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Search completed: October 11, 2004, 10:08:24 Job time : 1129.5 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using sw model OM nucleic

October 11, 2004, 08:24:41 ; Search time 189 Seconds (without alignments) 2966.995 Million cell updates/sec Run on:

Title: Perfect score:

US-10-009-317A-31 132 1 ggacctogtctactagtccc......cggttgacaatatttccgca 132 Sequence:

IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters:

6747726

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:* 1: geneseqn1980s:* Database :

genesequ2000s:* genesequ2001as:* genesequ2001bs:* genesequ2003s:* genesequ2003s:* geneseqn2003cs:* geneseqn2004s:* geneseqn1980s:* geneseqn1990s:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor. Plant yield-related polynucleotide clone G2520. ADD30447 standard; cDNA; 1197 BP. 09-AUG-2001; 2001US-0310847P. 19-NOV-2001; 2001US-0336049P. 11-DEC-2001; 2001US-0338692P. 14-JUN-2002; 2002US-00171468. 09-AUG-2002; 2002WO-US025805. (first entry) Arabidopsis thaliana. WO2003013227-A2. 15-JAN-2004 20-FEB-2003 ADD30447; RESULT 1 ADD30447

(MEND-) MENDEL BIOTECHNOLOGY INC.

Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE; Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu Broun PE;

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WPI; 2003-248221/24. P-PSDB; ADD30448.

New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate or apomixis.

Disclosure; SEQ ID NO 476; 454pp; English.

The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymorlectides and polypeptides are useful in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds, gene; transcription factor; transgenic plant; salt stress resistance; osmotic stress resistance; freezing tolerance; drought tolerance; low humidity tolerance; radiation resistance.
          modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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producing transgenic plants with commercially valuable properties,
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Pred. No. 0.37;
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19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-033692P.
14-UDM-2002; 2002US-00171468.
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56.3%;
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New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, i.e. modified desirable traits, e.g. salt stress resistance or tolerance

Disclosure; SEQ ID NO 37; 311pp; English

J, Pilgrim ML; Yu G, Broun PE;

Riechmann JL, Creelman RA, Keddie Jiang C, Ratcliffe O, Pineda O,

Heard JE, Dubell AN,

2003-248222/24.

WPI; 2003-248222/ P-PSDB; ADE31471.

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and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, e.g. salt stress resistance, osmotic stress resistance, tolerance to freezing, drought, low humidity tolerance, or radiation resistance. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention
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                                                                                                                                                                                                                           Sequence 1197 BP; 352 A; 224 C; 302 G; 319 T; 0 U; 0 Other;
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Pred. No. 0.37;
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2000US-00614150
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Best Local Similarity 56.3
Matches 58; Conservative
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P-PSDB; ABB68400.
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11-JUL-2000;
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ó 1524 GCCCCCCCCCAAAAGTTGGCCCCCCTGTACGTGTACGTATATCTGCTGCACCTTGGCGCCCCAGAA 1583 į The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention inseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell TTGCGGCGAGAA Gaps Drosophila melanogaster expressed polynucleotide SEQ ID NO 31988. developmental biology; cell signalling; insecticide; Sequence 6398 BP; 1456 A; 1470 C; 1528 G; 1944 T; 0 U; 0 Other; ; 0 . Match 22.4%; Score 29.6; DB 4; Length 6398; Local Similarity 61.8%; Pred. No. 2.5; les 47; Conservative 0; Mismatches 29; Indels 0; DB 4; Length 2817; Claim 1; SEQ ID NO 31988; 21pp + Sequence Listing; English. Match 22.4%; Score 29.6; DB 4; Length 2 Local Similarity 61.8%; Pred. No. 1.8; es 47; Conservative 0; Mismatches 29; Indels 1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTT EX. Myers BP. 1584 GGCGCACAGACATIC 1599 ABL12502 standard; cDNA; 6398 PWD, 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 16 23-MAR-2001; 2001WO-US009231 (first entry) GGCGAAAGTCTCAGTC ij pharmaceutical; gene; ss Drosophila melanogaster. Venter JC, Adams M, WPI; 2001-656860/75. P-PSDB; ABB68399. (PEKE) PE CORP NY WO200171042-A2 26-MAR-2002 Drosophila; 27-SEP-2001 61 ABL12502; Query Match Query Match XXX ABL12502/c
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79038 CTCGATGACACGTCAGCAACTAGCGAGAATCCGAGCCGGGAGTTCTGACGAACGCATTCG 78979 ö 64 CTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCG Sequence 82993 BP; 14881 A; 26628 C; 26719 G; 14765 T; 0 U; 0 Other; · 0 DB 6; Length 82993; Indels 22.1%; Score 29.2; DB 6; 157.8%; Pred. No. 10; 11ve 0; Mismatches 38; 78978 AACGCCCCCTGCCTCAACGAACAAGACGG 78949 65 AAAGTCTCAGTCGCTCTCCGAACTCCACGG 94 Query Match
Best Local Similarity 57.8'
Matches 52, Conservative В ò ò

This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species on a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and procective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a Mycobacterial cosmid DNA sequence used in the method of the invention

survival or virulence of mycobacteria the sequences of Mycobacterium

Identifying and selecting genes for s by a comparative genomic analysis of tuberculosis and M. leprae.

WPI; 2002-759885/82

Cole S;

22-FEB-2001; 2001US-0270123P.

(INSP) INST PASTEUR

22-FEB-2002; 2002WO-IB001973

Disclosure; Fig 4; 874pp; English

Mycobacterioses; survival; virulence, protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy; ds; cosmid.

Mycobacterium tuberculosis

WO200274903-A2.

26-SEP-2002

Aycobacterium tuberculosis H37Rv BAC clone BAC-Rv221

(first entry)

08-APR-2003

RESÚLT 5 ABX09140/c TD ABX09140 standard; DNA; 82993 BP.

2234 GGCGCACAGACATIC 2219

g ò

Sequence 2817 BP; 885 A; 722 C; 746 G; 464 T; 0 U; 0 Other;

X 8

16

61 GGCGAAAGTCTCAGTC

RESULT 6 AA199682_21/c ContinuaTion (22 of 45) of AA199682 from base 2100001 (Mycobacterium tuberculosis strain

2235

9

1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCCGGACTTTTGCGGCGAGAA 2294 decececenana de producer de la companie de la

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                                                                                                                                                                                                                                                                                         Length 110000;
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                                                                                                                                                                                                                                                                                                        38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C glutamicum coding sequence fragment SEQ ID NO: 2904.
                                                                                                                                                                                                                                                                                          Score 29.2; DB 4;
Pred. No. 11;
0; Mismatches 38;
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illarity 57.8%;
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800001
1000001
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11200001
1300001
1400001
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                                                                                                                                                                                                                                                                                                  Local Similarity
nes 52; Conserv
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AA199683_34
AA199683_38
AA199683_39
AA199683_41
AA199683_41
AA199683_43
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 LOCUS AAI99682 Accession Aai99682
                                                                                                                                                                                                                                                                                                                                                                     Score 29.2; DB 4; Length 110000; Pred. No. 11;
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300001
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Continuation (22 of 44) of A
WP Sequence split into 44 fr
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WP AA199683 02 20
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WP AA199683 04
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Matches 52; Conserv
 Sequence split into
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AA199682 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                 mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a research of a gene, measuring expression of a research of a gene, measuring expression of a research of a gene, measuring expression of a research of a gene a gene a research of a gene a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID NO 2904; 246pp + Sequence Listing; English.
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                                                                                                                                                          Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 21.8%; Score 28.8% Di Similarity 58.0%; Pred. No. 3.2; 51; Conservative 0; Mismatches
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                                                                                                                                                          Ando S,
                                                                                                                                                   Mizoguchi H, Ando
Senoh A, Ikeda M,
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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23-AUG-2000; 2000US-00649167.
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                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                                                                                                                                                                                                        WPI; 2001-376931/40.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          P-PSDB; AAG92650.
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                                                                                                                                                             Nakagawa S,
Tateishi N,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in game therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generic disorders or other traits to assess biodiversity red on to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the private of the invention of the contact of the contact sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brevibacterium lactofermentum sucrose PTS enzyme II DNA SEQ ID NO:1.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations rasponsible for genetic disorders or other traits and to assess biodiversity.
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62.5%; Pred. No. 3.2;
:ive 0; Mismatches
                                                                                                                                                                                             claim 1; SEQ ID NO 17093; 103pp; English.
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3779. .5764
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(first entry)
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Best Local Similarity 62.5;
Matches 45; Conservative
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20-APR-2001
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2001-639362/73. B; ABG17102. Φ

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Ikeda M,
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 Senoh A,
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AAI99682 12
ContinuaTion (13 of 45) of
WP Sequence split into 45
                                   WPI; 2001-376931/40.
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AA199682 01
AA199682 02
AA199682 03
AA199682 04
AA199682 06
AA199682 07
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AAI99682 15
AAI99682 16
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AAI99682_28
AAI99682_29
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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                                                                                                                                                                                                                                                                                                                                                     PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or bhosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and if's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                      Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                      present sequence encodes the Brevibacterium lactofermentum sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid synthesis, vitamin; saccharide;
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0
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Pred. No. 4.9;
0; Mismatches 37
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                                                                                                           Kurahashi O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3856 recaacecerracecercerecreaa 3883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AACTCCACGGAAACGTCTGCTCCAAA 112
                                                                                                                                                                                                                                                                                                    Claim 3; Page 22-29; 45pp; Japanese.
                                                                                                             Sugimoto M, Nakamatsu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH68533 standard; DNA; 349980 BP
 30-JUN-2000; 2000WO-JP004348
                                   99JP-00189512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino organic acid synthesis; ds.
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                                                                         (AJIN ) AJINOMOTO CO
                                                                                                                                               WPI; 2001-138150/14.
P-PSDB; AAB69080.
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                                   02-JUL-1999;
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of AA199682 from base 1200001 (Mycobacterium tuberculosis strain;
15 fragments LOCUS AA199682 Accession Aa199682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, meseuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and analysing and pacteria are useful for producing amino acids, nucleic acids, vitamines, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7068; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111729 recaacecerrracecercerericaaa 111702
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Ozaki A;
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45607 GACTITCGCCAACAAGGCGCTGTCGCGATGCGCAAGCAGTTCGGCGGACACGCCGAGAAA 45666
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                                                                                                                                                                                                                                                                                                                              A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.
                                                                                                                                                                                                                                                                                                                                               TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter; glaucoma; steroid sensitivity; progressive ocular hypertension; vision loss; ss.
                                                                                                                      2 GACCICGICIACIAGICCCTIACCGAGIAAGGAAAIGIGCCGGACTITIGCGGCGAGAAG
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis, prognosis and treatment of glaucoma, based on detecting specific polymorphisms in the promoter of the trabecular meshwork inducible glucocorticoid receptor gene.
                                                                     Score 28.4; DB 4; Length 110000;
Pred. No. 23;
0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "GTGT added to produce TIGRmt3 mutant"
replace(5113, C)
                                                                                                                                                                                   45667 CCGGCTAACTAAGTCGCCTGACGAAGTCCACCACGACGTCGG 45708
                                                                                                                                                                    . 62 GCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTG 103
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/note= "TIGRmt11 mutant"
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/note= "TIGRmt4 mutant"
replace(4337, G)
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/note= "TIGRmt1 mutant"
replace(4950, T)
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/note= "TIGRmt2 mutant"
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replace(4256, G)
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99US-00306828.
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ilarity 54.9%;
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4300001
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Best Local Similarity
AA199683_39
AA199683_40
AA199683_41
AA199683_42
AA199683_43
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07-MAY-1999;
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                                                                                                                                                                                                                                             2 GACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAG 61
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                             Score 28.4; DB 4; Length 1 Pred. No. 23; 0; Mismatches 46; Indels
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Local Similarity 54.9%;
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Continuation (13 of 44) of AA
WP Sequent Into 44 fra
WP Sequent Same
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WP AA199683_01
WP AA199683_04
WP AA199683_05
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AA199682 34
AA199682 43
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Matches
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glucocorticoid receptor) promoter, isolated from an individual without glucocorticoid receptor) promoter, isolated from an individual without prognosis and treatment of glaucoma. Dased on detecting specific polymorphisms in the promoter of the TIGR gene. The method is used for diagnosis and prognosis of glaucoma (of all types), steroid sensitivity and progressive ocular hypertension that leads to loss of vision. Glaucoma can be treated by administering an agent that binds to cisculatory regions) can be used to express homologous or heterologous genes, particularly for tissue-specific expression of therapeutic transgenes for treating glaucoma, also to generate transgenic animals and in screening for compounds (specific modulators) with diagnostic or therapeutic potential. Fragments of the TIGR sequence can be used as amplification primers or probes, e.g. for isolating related sequences in
meshwork inducible
   present sequence represents a TIGR (trabecular
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Gaps Sequence 5271 BP; 1476 A; 1138 C; 1231 G; 1426 T; 0 U; 0 Other; .; o Score 27.6; DB 3; Length 5 Pred. No. 13; 0; Mismatches 39; Indels Query Match 20.9%; Best Local Similarity 56.7%; Matches 51; Conservative

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2040 Tratreagractratarcreceaeacaceaeacaeaacaaaareereaeaaceaaaceaere 21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC 81 TCCGAACTCCACGGAAACGTCTGCTCCTCA 110 d ò . 유 à

2100 cccraccrrceredagereacacrircrca 2129

AAV51361 standard; DNA; 5299 BP RESULT 1: AAV51361 ID AAV5

AAV51361;

Human TIGR promoter region DNA.

(first entry)

27-OCT-1998

diagnosis; glaucoma; polymorphism; steroid sensitivity; ss trabecular meshwork induced glucocorticoid TIGR;

protein; human;

Homo sapiens

WO9832850-A1.

09-JAN-1998; 30-JUL-1998

98WO-US000468

97US-00938669. 28-JAN-1997; 26-SEP-1997;

(REGC) UNIV CALIFORNIA

Chen H;

Chen P,

Polansky JR,

Nguyen TD,

WPI; 1998-427946/36.

Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma.

Claim 34; Fig 1; 105pp; English.

This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGR) promoter region which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can

2040 rrarreagractrararcreceagacacegadacaaaregregagecaaacadrecre 2099 21 ITACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAAGTCTCAGTCGCTC Gaps Sequence 5299 BP, 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other; .; 0 Length 5299; DB 2; 2100 cccraccircgredaggredacagrircica 2129 Pred. No. 13; 0; Mismatches Score 27.6; Pred. No. 13 81 TCCGAACTCCACGGAAACGTCTGCTCCTCA also be used to diagnose glaucoma 20.9%; 56.7%; Conservative Local Similarity 51; Query Match Matches ន្តដូល 셤 ઠ ઠ

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Search completed: October 11, 2004, 09:30:40 Job time : 191 secs

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Tue Oct 12 09:20:50 2004
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                                                                                                                                                October 11, 2004, 09:19:46; Search time 39.5 Seconds (without alignments) 1854.519 Million cell updates/sec
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US-09-309-487-31

i Sequence 31, Application US/09309487

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j Patent No. 6335318

i GENERAL INFORMATION:

j APPLICANT: Selected, Michael E.

APPLICANT: Year, Jun

APPLICANT: Year, Jun

APPLICANT: Obellette, Andre J.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FIRE REFERENCE: P-UC 3095

CURRENT APPLICANT: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 31

LENGTH: 132
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
FOTHER INFORMATION: CONStruct
CALOR INFORMATION: CONSTRUCT
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100.0%; Score 132; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-39;
Matches 132; Conservative 0; Mismatches 0; Indels
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US-09-967-808-31
Sequence 31, Application US/09967808
Sequence 10. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Cuan
APPLICANT: Yuan, Jun
APPLICANT: Vuen, Jun
APPLICANT: Vuen, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using TITLE OF INVENTION: Same FILE REFERENCE: P-UG 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 132
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Construct
US-09-309-487-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 132; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-39;
Matches 132; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 30, Application US/09309487; Patent No. 6335318; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA . ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATATTTCCGCA 132
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US-09-309-487-30
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LENGTH: 132
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121 AATATTTCCG 130

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Sequence 30, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Town, Jun

APPLICANT: Power Information of Using

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using

TITLE OF INVENTION: Same

FILE REFERENCE: P-UC 3095

CURRENT APPLICANTON NUMBER: US/09/967,808

CURRENT APPLICATION NUMBER: US/09/309,487

PRIOR APPLICATION NUMBER: US/09/309,487

PRIOR APPLICATION NUMBER: US/09/309,487

SOFTWARE: PALENTIN Ver. 2.0

SEQ 1D NO 30

LENGTH: 132
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COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FARSER, Claire M.
APPLICANT: FARSER, Claire M.
APPLICANT: VERYER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBRECULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.7%; Score 109.2; DB 4; Best Local Similarity 90.0%; Pred. No. 5.2e-31; Matches 117; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AATATTTCCG 130
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US-09-103-840A-2/c
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US-09-103-840A-2

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2191948 CTCGATGACACGTCAGCAAACTAGCGAGATCCGAGCCGGAGTTCTGACGAACGCATTCG 2191889
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Sequence 2, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, John C.

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24566-20007.00

CURRENT APPLICATION UNBER: US/09/103,840A

CURRENT PILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                    5 CTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGAACTTTTGCGGCGAGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CICGICIACIAGICCCITACCGAGIAAGGAAAIGIGCCGGACTITIGCGGCGAGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VORTER, Claire M.
APPLICANT: VORTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1.
LENTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.1%; Score 29.2; DB 3; Length 4411529; Best Local Similarity 57.8%; Pred. No. 8.5; Matches 52; Conservative 0; Mismatches 38; Indels 0;
  Length 4403765;
                                                     38; Indels
  DB 3;
                                                                                                                                                                                                                                                 2194589 AACGGCCCCGTGCCTCAACGACAAGACGG 2194560
Query Match .22.1%; Score 29.2; DE
Best Local Similarity 57.8%; Pred. No. 8.5;
Matches 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 AAAGICICAGICGCICICCGAACICCACGG 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHEN INFORMATION: H37Rv
US-03-103-8408-1
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 629428 GENERAL HORMATION: APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-103-840A-1/c
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RESULT 9
US-09-306-828-34
US-09-306-828-34
Squence 34 Application US/09306828
Squence 34 Application US/09306828
Squence 34 Application US/09306828
Squence 34 Application US/09306828
Squence 34 Application US/09/08
APPLICANT: NGUYANTION:
APPLICANT: Chen, Hua
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis And
TITLE OF INVENTION: Nucleic Acids, US/09/306,828
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT APPLICATION NUMBER: US/09/207,881
BARLIER FILING DATE: 1999-01-11
NUMBER OF SEO ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 34
LENGTH: 5271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1246078 GACTTCGCCAACAAGGCGCTGTCGCGATGCGCAAGCAGTTCGGCGGACACGCCGAAAA 1246137
                                                                                                                                                       1245607 GACTTCGCCAACAAGGCGCTGTCGGCGATGCGCAAGCAGTTCGGCGGACACGCCGAGAA 1245666
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GENERAL INFORMATION:
APPLICANT: FLEISCHTAN, Robert D.
APPLICANT: PRASER: Claire M.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
CURRENT APPLICATION NUMBER: U5/09/103,840A
CURRENT APPLICATION NUMBER: U5/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                           2 GACCTCGTCTACTACTCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAG
                                                         0; Gaps
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Score 28.4; DB 3; Length 4403765;
Pred. No. 16;
0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                             1245667 CCGGCTAACTAAGTCGCCTGACGAGTCCACCACGACGTCGG 1245708
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                                                                                                                                                                                                                 62 GCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GCGAAAGICICAGICGCICICCGAACICCACGGAAACGICIG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.5%; Score 28.4; DB 3; Best Local Similarity 54.9%; Pred. No. 16; Matches 56; Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
THER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
        Query Match
Best Local Similarity 54.9%;
Matches 56; Conservative (
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CRGANISM: Homo sapiens
US-09-306-828-34
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RESULT 12
US-08-938-669A-2
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                                                                                                                                       2040 TTATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTG 2099
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                                                                                           21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC
                                                Gaps
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Query Match 20.9%; Score 27.6; DB 4; Length 5271; Best Local Similarity 56.7%; Pred. No. 2.6; Matches 51; Conservative 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, On R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: MELATED DISEASES
NUMBER OF SEQUENCES: 3.2
CORRESPONDENCE ADDRESS:
ADDRESSE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.9%; Score 27.6; DB 3; Length 5300; 56.7%; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                     2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2100 cccraccrrceredaggreacagrirerca 2129
                                                                                                                                                                                     81 TCCGAACTCCACGGAAACGTCTGCTCCTCA 110
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CLASSIFICATION 435
PRICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Biliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202 383-6857
                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08938669A
Patent No. 6171788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5300 base pairs TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear US-08-938-669A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-938-669A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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RESULT 11

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Patent No. 6475724
GENERAL INFORMATION:
Patent No. 6475724
GENERAL INFORMATION:
BAPLICANT: Mayuen, Thai D.
APPLICANT: Chen, Pu
APPLICANTION: NUMBER: US/09/306, 828
CURRENT FILING DATE: 1999-05-07
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE NEW INCOSOFT WORD 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 27.6; DB 4; Length 5300; 56.7%; Pred. No. 2.6; tive 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NGUYEN, Thai D.
APPLICANT: NGUYEN, Thai D.
APPLICANT: NGUYEN, TON R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWIEY & Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 2004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FESTESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Howrey & Simon
: 1299 Pennsylvania Avenue, N.W
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07425-0034
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FILING DATE:
FILING DATE:
CLASSIFICATION: 435
RAIOR APPLICATION DATA:
APPLICATION NUMERS: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: 9-42,878
REFERENCE/DOCKET NUMBER: 07425-(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08938669A; Patent No. 6171788; GENERAL INFORMATION:
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TELEX:
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.7<sup>3</sup>
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                                                                                               ; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-1
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US-09-306-828-3

US-09-306-828-3

US-09-306-828-3

Sequence 3, Application US/09306828

Patent No. 6475724

GENURAL INFORMATION

APPLICANT: NGUVAN: Thai D.

APPLICANT: Chen, Hua

APPLICANT: Chen, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAGGCGAAAGTCTCAGTCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 6169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
SUPPLYARE: FastERO for Windows Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
TELLEPAN: 202 383-6610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2100 cccracchrcereaagaraacagrirchca 2129
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Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.9%;
Best Local Similarity 56.7%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
Matches 51; Conserv
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US-09-306-828-2

Sequence 2, Application US/09306828

Patent No. 6475724

GENERAL INFORMATION:
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hu
APPLICANT: Chen, Hu
APPLICANT: Chen, Hu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT FILING DATE: 1999-05-07

CURRENT FILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Microsoft Word 97

SEQ ID NO 2

LENGTH: 5304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2040 Tratrgagractrararcrgccagacaccagagacaaarcgrgagcaaagcagrcacrg 2099
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                                                                                                                                                                                                                                                                                                                             21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC
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                                                                                                                                                                                                                Length 5304;
                                                                                                                                                                                                          Query Match 20.9%; Score 27.6; DB 3; Length 5
Best Local Similarity 56.7%; Pred. No. 2.6;
Matches 51; Conservative 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2100 cécracérrégrégagaréacagríficiéa 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                            81 TCCGAACTCCACGGAAACGTCTGCTCCTCA 110
            SEQUENCE CHARACTERISTICS:
LENGTH: 5304 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPDLOGY: linear
US-08-938-669A-2
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2100 CCCTACCTTCGTGGAGGTGACAGTTTCTCA 2129 gg

Search completed: October 11, 2004, 10:56:45 Job time: 51.5 secs

Sequence 66646, A
Sequence 3539, A
Sequence 34, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1228, App
Sequence 1228, App
Sequence 1259, App
Sequence 264, App
Sequence 230, App
Sequence 11323, App
Sequence 1139, App
Sequence 229, Appl

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221
643
200
5200
5300
5300
5304
6169
37252
4026
217409
October 11, 2004, 10:08:26; Search time 214 Seconds (without alignments) 3127.023 Million cell updates/sec
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                                                                                                                           US-10-009-317A-31
132
1 ggacctcgtctactagtccc......cggttgacaatatttccgca 132
                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/DSO7 PUBCOMB seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/DSO6 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*

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10: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

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14: /cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

15: /cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*

16: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*

17: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*

18: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*

18: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*

19: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*

19: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               3340653 seqs, 2534783454 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                            IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                            length: 0
length: 200000000
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Perfect score:
                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                            Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                     Sequence:
                                                                                                                                                                                                               Searched:
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ALIGNMENTS

US-10-113-994-31

Sequence 31, Application US/10313994

Sequence 31, Application US/10313994

Publication No. US20030162718A1

APPLICANT: Seleted, Michael E. APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Vuan, Jun

APPLICANT: Vuan

APPLICANT: ö 120 120 9 9 GGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGAC 1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGGGAGAAA 1 GGACCTCGTCTACTAGTCCCTTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAA GGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGAC 0; Gaps CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-313-994-31 Length 132; Indels Query Match 100.0%; Score 132; DB 15; Best Local Similarity 100.0%; Pred. No. 1.7e-40; Matches 132; Conservative 0; Mismatches 0; TYPE: DNA ORGANISM: Artificial Sequence FEATURE: 61 61 g g 8 $\stackrel{>}{\circ}$

Sequence 31, Appl Sequence 30, Appl Sequence 47, Appl Sequence 443, Appl Sequence 645, Appl Sequence 645, Appl Sequence 2175, Appl Sequence 2004, Appl Sequence 1, Appli Sequence 262, Appli Sequence 3528, Appli

5 US-10-313-994-31 5 US-10-215-066A-479 6 US-10-225-066A-479 6 US-10-225-067-37 5 US-10-205-067-37 6 US-10-374-780A-443 7 US-10-080-170-645 6 US-10-369-493-36378 US-09-738-626-294 9 US-09-738-626-1 5 US-10-198-846-9562 6 US-10-369-493-34295 6 US-10-369-493-34295

1132 1132 11132 11132 11132 11132 11132 11132 11132 11133 11133 1113 11

1000.0 82.7 82.7 23.5 23.5 23.5 22.1 22.1 22.0 21.8 21.8 21.8 21.5 21.5

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Description

Length DB

Query Match

Result No.

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PRIOR APPLICATION NUMBER: 60/310,04,
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: Patentin Version 3.1
SEQ ID NO 479
LENGTH: 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10225067
Publication No. US20040019925A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 56.3%;
Matches 58; Conservative
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1 NAME/KEY: CDS

1 LOCATION: (133)...(1197)

US-10-225-067-37
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APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, Omara
APPLICANT: PINEDA, Omara
APPLICANT: YU, Guo-Liang
APPLICANT: YO, Sierre
APPLICANT: PROUN, Pierre
TITLE OF INVENTION: Yiela-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Yi-Charles E.
APPLICANT: Tang, Yi-Charles E.
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Vuan, Jun
APPLICANT: Outsiles, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFRENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/10/313,994
CURRENT FILING DATE: 2002-12-05
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCTGCTCCTCAAACGGTTGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGTGAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-313-994-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.7%; Score 109.2; DB 15; Length 132; 90.0%; Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 479, Application US/10225066A Publication No. US20030226173A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mendel Biotechnology, Inc. APPLICANT: AAPLICANT: AAPLICANT: ALECHMANN, Jose Luis APPLICANT: ADAM, Luc J d APPLICANT: HOBELL, ARNOL T AAPPLICANT: HOBEL, ARNOL AAPLICANT: HOBEL, ARNOL AAPLICANT: HOBEL, ARNOL AAPLICANT: HOBEL, ARNOL AAPLICANT: PILGRIM, MATSHA L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                                                                      Sequence 30, Application US/10313994
Publication No. US20030162718A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                         121 AATATTTCCGCA 132
                                                                                      121 AATATTTCCGCA 132
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Best Local Similarity 90.0
Matches 117; Conservative
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121 AATATTACAG 130
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US-10-225-066A-479
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US-10-313-994-30
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APPLICANT: Heard, Jacqueline E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Creelmann, Robert A.
APPLICANT: Creelmann, Robert A.
APPLICANT: Keddie, James
APPLICANT: Manole I.
APPLICANT: Dibell, Arnold T.
APPLICANT: Bineda, Omaira
APPLICANT: Prineda, Omaira
APPLICANT: Prineda, Omaira
APPLICANT: Bineda, Omaira
APPLICANT: Dibell, Arnold T.
APPLICANT: Dibell, A
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Pred. No. 0.24;
0; Mismatches 45; Indels 0
Query Match
23.5%; Score 31; DB 13; Length 1197;
Best Local Similarity 56.3%; Pred. No. 0.24;
Matches 58; Conservative 0; Mismatches 45; Indels
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US-10-080-170-645/c

US-10-080-170-645/c

Sequence 645, Application US/10080170

Sequence 645, Application US/10080170

Sequence 645, Application US/2004012132289

GENERAL INFORMATION:

TITIE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 645

LENGTH: 82993
                                         Sequence 645, Application US/10080170
; Sequence 645, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INPORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: DENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; TITLE OF INVENTION: UNBER: US/10/060,170
; CURRENT FALING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; RIOR APPLICATION NUMBER: 60/270,123
; RIOR PILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 645
; LENGTH: 82993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.1%; Score 29.2; DB 17; Best Local Similarity 57.8%; Pred. No. 3.9; Matches 52; Conservative 0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 AAAGTCTCAGTCGCTCTCCGAACTCCACGG
                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; CORGANISM: Mycobacterium tuberculosis
US-10-080-170-645
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TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC 80
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                                                                                                  1047 TAAGCATTGCAATGAACCGTTTGGTCAGCAAGCGTTTGAGAAT 1089
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                                                                           81 TCCGAACTCCACGGAAACGTCTCCTCCAAACGGTTGACAAT 123
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Publication No. US20040019927A1
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ORGANISM: Arabidopsis thaliana
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CTHER INFORMATION: G2520
US-10-374-780A-443
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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ilarity 58.0%;
Conservative
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                               APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HAKUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: KEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HAWUHIKO
TATEISHI, NAOKO
IKEDA, MKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                     US-09-738-626-2904
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US-09-738-626-1/C
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APPLICANT:
APPLICANT:
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Matches
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US-10-369-493-36378/C

Sequence 36378, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICHOBIAL PROPERINS
FILE REFERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 1739
US-10-062-674-2175/c

| Sequence 2175, Application US/10062674
| Publication No. US20040005559A1
| Publication No. US20040005559A1
| GENERAL INFORMATION:
| APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
| TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
| FILE REPERENT PILICATION NUMBER: US/10/062,674
| CURRENT PILICATION NUMBER: US 09/625,102
| PRIOR APPLICATION NUMBER: US 09/625,102
| PRIOR PILING DATE: 2002-01-30
| PRIOR PILING DATE: 2000-07-24
| NUMBER OF SEQ ID NOS: 2217
| SEQ ID NO 2 175
| LENGTH: 5493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
21.8%; Score 28.8; DB 16; Length 1
Best Local Similarity 58.0%; Pred. No. 1.9;
Matches 51; Conservative 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 814967.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure

; LOCATION: (1) ... (5493)

; OTHER INFORMATION: a, t, c, g, or other

US-10-062-674-2175
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; ORGANISM: Aspergillus nidulans
US-10-369-493-36378
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Pred. No. 1.9;
0; Mismatches
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APPLICANT: TAMESHI, MACKO
APPLICANT: SENCH, MASHTO
APPLICANT: SENCH, MASHTO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
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                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                 APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/317484
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 2904
LENGTH: 1983
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
Sequence 2904, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; Corynebacterium glutamicum
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2904
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Query Match 21.5%; Score 28.4; DB 16; Best Local Similarity 60.3%; Pred. No. 2.9; Matches 47; Conservative 0; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Desulfitobacterium hafniense
US-10-369-493-33481
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; Sequence 66646, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2168 ACCGGGCCGGAATTAAAC 2185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               513 GCGGGGAGCAGGAACCGGCTCAGATACCCTTCCACACCCGTGGAAACTTTTGTTCTTTA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-198-846-9562/c
| Sequence 9562, degree 9622, degree 96222, degree 962222, degree 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 CGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAAGTCTCAGTCGCTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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| NAME/KEY: misc_feature
| NAME/KEY: misc_feature
| LOCATION: 3, 562, 567, 597, 615, 621, 651, 656, 660, 667, 679, 682,
| LOCATION: 690, 707, 723, 724, 753, 762, 790, 794, 795, 796, 799, 800,
| LOCATION: 811, 819, 835, 866, 878, 879, 882
| OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                   Length 3309400;
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                                                                                                                                                                                                                                                                                                                                                                                                                            37; Indels
                                                                                                                                                                                                                                                                                                                                           Query Match
21.8%; Score 28.8; DB 9;
Best Local Similarity 58.0%; Pred. No. 16;
Matches 51; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2811729 TGCAACGCGTTTACGCCTCGTGCTCAAA 2811702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AACTCCACGGAAACGTCTGCTCCTCAAA 112
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9.10-369-493-33481
9.8cquence 33481, Application US/10369493
9.Publication No. US20030233675A1
9.GENERAL INFORMATION:
9.APPLICANT: Cao, Yongwei
9.APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                          TYPE: DNA; OCKGANISM: Corynebacterium glutamicum US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AACGGTTGACAATATTTC 128
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
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Sequence 34295, Application US/10369493
; Sequence 34295, Application US/10369493
; Sequence 34295, Application No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongword
; APPLICANT: Glaman, Barry S.
; APPLICANT: Glaman, Barry S.
; APPLICANT: Glaman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EARLY S.
; EARLY S
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Earry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EARNESSION OF MICROBIAL PROPERTIES
FILE REPERRORE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SRQ ID NO 33481
LENGTH: 2301
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21.2%; Score 28; DB 16; Length 2574;
Best Local Similarity 52.6%; Pred. No. 4.2;
Matches 61; Conservative 0; Mismatches 55; Indels (
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 6646
ILENGTH: 221
TYPE: DNA
ORGANISM: Glycine max
PREAUME: COMBREMISM: Glycine max
OTHER INFORMATION: Clone ID: PAT_MRT3847_31195C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GCCGGACTTTTGCGGCGAGAAGCCGAAAGTCTCAGTCGCTCTCCGAACTCCCACGGAAACG 99
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21.1%; Score 27.8; DB 13; Length 221;
Best Local Similarity 57.5%; Pred. No. 2.5;
Matches 50; Conservative 0; Mismatches 37; Indels 0;
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Search completed: October 11, 2004, 12:14:35 Job time : 217 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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October 11, 2004, 08:56:11; Search time 1398.5 Seconds (without alignments) 2818.597 Million cell updates/sec sw model - nucleic search, using OM nucleic Run on:

US-10-009-317A-31 132 1 ggacctcgtctactagtccc......cggttgacaatatttccgca 132 Perfect score: Sequence:

Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:*

em estba:*
em estbum:*
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gb htc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		BF088574 RC1-HT088	AA757359 ah96d12.s	BX437353 BX437353	AA392125 LD12495.5
		O.		BF088574	397 9 AA757359	BX437353	AA392125
		DB	1	10	σ	13	σ
		Match Length DB	1 1 1 1 1 1 1				
dю	Query	Match	1 1 1 1 1 1 1 1 1 1	24.4	30.4. 23.0	22.7	22.4
		Score		32.2	30.4	30	29.6
	Result	No.		Н	7	m	4
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00488		20,000,00	10 4 H W 10 -	0 1 2 2 1 4 4 0 8 4 4	1892 1007 1007 1008 1008 1008 1008 1008 1008	941892 LD2722 A361075 63482 L455487 T. br C194385 CH261 60849 TGESTZY
	A	10000	4 M O M 6	10001	3306	32566 HS_5004_ 33067 tigr-gss 57825 HSC 0026 96609 BX396609
	000000	,	200W4W	101100	00000000	30829 ZMMBBb0 30829 ZMMBBb0 35601 6018685 79821 6025273 33040 6015695 38814 6010946
2 2 2 2 2 2 2 4 2 4 2 4 4 4 4 4 4 4 4 4			714004	22 H 1 0 H 2 8 4 4 6 4 4 6 4 4 6 4 6 4 6 6 6 6 6 6 6	22080140 22086140	30144 BOHSU4 30144 BOHSU4 58652 tricol 58747 tricol 2208 TGESTZZ 562 TGESTZY7
			4 10 10 12 10 00 0		1836 1757 289 726	995.6 IGESTZYE 1836 TGESTZZ47 17576 TGESTZY1 103 TGESTZY86e 289 TGESTZY45e
o t a a o u u u u u u u	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	221.5 221.5 221.5 221.5 221.5 221.5	4 4 4 4 4 4 4 4 4 5 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1001111111 0 4044444	AW703408 AA012485 AA012483 N69183 N69183 T6236 N8138 CA96851 CA961517	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Materia, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Meteria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 193)
Dias Neto,E., Garcia,Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., BF088574 130900-014-bl1 HT0881 Homo sapiens cDNA, mRNA sequence. BF088574.1 GI:10894284 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 RESULT 1
BF088574/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CETWORDS
SOUNCE
ORGANISM JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS TITLE

Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

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22.7%; Score 30; DB 13; Length 951; larity 45.9%; Pred. No. 99; Conservative 17; Mismatches 23; Indels
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BX437353.1 GI:30777557
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Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Best Local S:
Matches 58
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BX437353/c
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
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                                                                                                                                                                                                                                                                  /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="mRNA"

/db_xref="Adult"

/clone_lib="HT0881"

/clone_lib="HT0881"

/clone_forgan: head_neck, Vector: puc18; Site_l: Smal;

/note="Organ: head_neck, Vector: puc18; Site_l: Smal;

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector: Reverse transcription of

tissue mRNA and cnDNA amplification were performed under

low stringency conditions."
                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCl-HT0891-130 900-014-bl1&t3=2000-09-13&t4=1) Seq primer: puc 18 forward High quality sequence start: 28 High quality sequence start: 28 High quality sequence stop: 192.
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1 (Dases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Bmail: Gapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 478 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA757359 397 bp mRNA linear EST 31-DEC-1
ah96d12.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1326935 3' Similar to gb:X59357 60S RIBOSOMAL PROTEIN L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ACCICAACICCIGGCICAAIACIGAIGGAAGIAAICIGCIIAACAAICICAGAAGGACIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAAGTCATGGTCGCTTGTGATTCTCAACTGAAACGAGGGATCCTCTA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.2; DB 10; Length Pred. No. 11; 0; Mismatches 48; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_aref="IMAGE:1326935"
/lab_host="DH108"
/clone_lib="Soares_NFL_T_GBC_S1"
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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AA757359
AA757359.1 GI:2805222
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56.0%;
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Matches 61
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL)9W, testis NH7, and B-cell NCL_CGAP_CCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="Taxon:9666"
/clone="CSOCAPOG5VO24"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
the Not I and ECRNY sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 TTACCGAGTAAGGAAATGTGCCGGACTTTTGCGGCGAGAAGGCGAAAGTCTCAGTCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 23.0%; Score 30.4; DB 9; Length 397; I Similarity 55.8%; Pred. No. 52; 58; Conservative 0; Mismatches 46; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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Gaps

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us-10-009-317a-31.rst

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Tue Oct 12 09:20:50 2004
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CTTTTGCGGCGAGAA : : : CYTKGGCGKGTGGAI CCTCAAACGGTTGA	Db 888 TGAACAACSGTTCA 875	RESULT 4 AA392125 LOCUS LOCUS AA392125 DEFINITION LD12495.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD12495 5prime, mRNA sequence. ACCESSION AA392125 VEGETON AA302125	VERSION AA392125.1 GI:2045119 KEYWORDS EST. SOURCE Drosophila melanogaster (fruit fly) SOURCE ORGANISM melanogaster ORGANISM melanogaster ORGANISM brosophila melanogaster Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Enhydroidea; Drosophilidae; Drosophila. Ephydroidea; Drosophilidae; Drosophila. REFERENCE I (bases 1 to 315) AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., TITLE JOURNAL COMENT Contect: Stapleton, M. COMMENT BDGP	Cyclot Cyclot 510 4 1: htt P elem quali	/clone="LD12495" /sex="male and female" /dev_stage="0 to 24 hours mixed stage embryonic" /lab_host="SOLM" /clone_lib="ID Drosophila melanogaster embryo BlueScript" /note="Organ: embryo; Vector: BlueScript SK; Site 1:	Query Match 22.4%; Score 29.6; DB 9; Length 315; Best Local Similarity 61.8%; Pred. No. 86; Matches 47; Conservative 0; Mismatches 29; Indels 0; Gaps 0; Qy 1 GGACCTCGTCTACCGGGAAAATGTGCCGGACTTTTGCGGCGAGAA 60 Db 197 GGCCGCGGAAAAGTTGGCCCTGTACGTGTACGAAATATCTGCTGCACGAAA 256	OY 61 GGCGAAAGTCTCAGTC 76 	RESULT 5 AQ034104 LOCUS LOCUS 1(3)neo48 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

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1. .484
/organism="brosophila melanogaster"
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/clone_lib="brosophila melanogaster P lethal line"
/note="finverse PCR was performed on brosophila
melanogaster strains each of which contains a single P
rransposable element insertion that is thought to cause
either lethality or sterility. The resultant fragment for
each strain was directly sequenced to determine the
genomic sequence at the site of insertion. Details of the
protocols used can be found at
http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The P element insertion position is base 001 in the 484 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
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                                                                                 Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryorta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryorta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bohydroidea; Drosophildae; Drosophila.

Ephydroidea; Drosophildae; Drosophila.

(Bases 1 to 484)

Espradling, A.C., Stern, D., Beaton, A., Rehm, E.J., Laverty, T., Mozden, N., Misra, S. and Rubin, G.M.

Mozden, N., Misra, S. and Rubin, G.M.

The BDGP gene disruption project: Single P element insertions mutating 30% of Drosophila autosomal genes

Unpublished (1998)

Contact: Gerald Rubin

Berkeley Drosophila Berkeley

LSA Building, Berkeley, CA 94720-3200, USA

Fax: 5106439947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
                      AQ034104.1 GI:3293724
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/clone="LD43627"

/clone="LD43627"
/dev stage="0 to 24 hours mixed stage embryonic"
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/lab_host="XL1 Blue"
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/note="Organ: embryo; Vector: pOT2; Site_1: EcoR1; Site_2:
Xhot; Sized fractionated cDNAs were directly ligated into pOT2.
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LD37723.Sprime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD37723 Sprime, mRNA sequence.
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/lab_bost="%XL1 Blue"
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/clone="Organ: embryo; Vector: pOT2; Site_1: EcoR1; Site_2:
Xho1; Sized fractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 GGCCCGCGAAAAGTTGGCCCCTGTACGTGTACGAATATCTGCTGCACGTTGGCGCCCAGAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Enkaryota; Encaperygota; Ditera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 609)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Bocey-HHMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC006495; hit P element sequence 1(3)neo48
Plate: 377 row: B column: 11
High quality sequence stop: 500.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                             Length 578;
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                                                                                                                                                                                                                                                                                                                                                                                             ch 22.4%;
1 Similarity 61.8%;
47; Conservative (
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/dev stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/clone_lib="LD brosophila melanogaster embryo pOT2"
/note="Organ: embryo; Vector: pOT2; Site 1: EcoR1; Site 2:
Xhoi; Sized fractionated cDNAs were directly ligated into
pOT2.
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LD43627.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD43627 5prime, mRNA sequence.
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                                  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC006495; hit P element sequence 1(3)neo48
Plate: 441 row: D column: 10
High quality sequence stop: 522.
Location/Qualifiers
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hit genomic sequence ACO06495
hit genomic sequence ACO06495
Plate: 436 row: C column: 3
High quality sequence stop: 446.
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/mol_type="mRNA"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LD44146"
                                                                                                                                                                           Contact: Stapleton, M. BDGP
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   (bases 1 to 555)
                                                                                                                                         Unpublished (2001)
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 15A, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 GGAAATGTGCCGGACTTTTGCGGCGAGAGGCGAAAGTCTCAGTCGCTCTCCGAACTCCCA 91
                                                                                                                                                                                                                                                                                                                                     Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified b
cross match v0.990329.
Seq primer: AGCGGATAACATTCACACAGGA.
Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus.
                              1 (bases 1 to 244)
Rexroad,C.E. and Keele,J.W.
Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
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T. brucei sheared genomic DNA clone 41cOS, reverse sequence,
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Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.1%; Score 29.2; DB 14;
llarity 62.2%; Pred. No. 16+02;
Conservative 0; Mismatches 28;
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Email: nelsayed@tigr.org
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Matches 46; Conserv
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LD27222.Sprime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD27222 Sprime, mRNA sequence.
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Oncorhynchus mykiss
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

1 (bases 1 to 750)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Lawrence Berkeley, CA 94720, USA
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit P element sequence 1(3)neo48-3[001],
Plate: 272 z ow: B column: 10
High quality sequence stop: 627.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7227"
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                                                                        268 ĠĠĊĠĠĊĄĊĄĠĄĊĄTŢĊ 283
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                                     GGCGAAAGTCTCAGTC
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VERSION KEYWORDS SOURCE ORGANISM

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N60849.1 GI:1207000
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
_bocation/Qualifiers
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1 (bases 1 to 1135)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Gallus gallus BAC End Reads

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_l: BcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
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                                                                                                                                                                                                     22.1%; Score 29.2; DB 29; Length 517; 52.5%; Pred. No. 1.4e+02; ive 0; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                     /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/srrain="TREU927"
/db_xref="taxon:5691"
/clone="41005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends
High quality sequence start: 127
High quality sequence stop: 556.
Location/Qualifiers
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Best Local Similarity 52.5°
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CC194385
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/db_xref="taxon:5811"
/db_xref="taxon:5811"
/dlob_bost="taxon:5811"
/lab_host="taxon:5811"
/lab_host="taxon:1811"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 bp mRNA linear EST 22-MAY-200 TGSST2Y23h01.rl TGRH Tachyzoite cDNA Toxoplasma gondii cDNA clone tgzy23h01.rl 5' similar to SW:Rl6C_ORYSA P46294 40S RIBOSOMAL PAROTEIN S16: ;, mRNA sequence.
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David Sibley at toxoest@borcim.wustl.edu for further information
relating to organism, clone or library availability.
Seq primer: T3
High quality sequence stop: 224.

Location/Qualifiers
| . 354 |
/organism="Toxoplasma gondii" |
/mol_type="mRNA" |
/strain="RNA" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxoplasma gondii
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.

( bases I to 354)
Hehl,A., Manger,I., Marra,M., Sibley,L.D., Ajioka,J.A.,
Aslett,M.A., Dietrich,N., Dubuque,T., Hillier,L., Kucaba,T.,
Wan,K.L., Waterston,R.H. and Boothroyd,J.
Unpublished (1996)
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%; Score 29; DB 14; Length 354;
larity 62.9%; Pred. No. 1.40+02;
Conservative 0; Mismatches 26; Indel8
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completed: October 11, 2004, 10:55:09
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Menatacoa; Nematoda; Chromadorea; Rhabditida;
Enhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (Dases 1 to 412)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Harnerong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Ptecek, J., Snyder, M., Hudang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 06-MAR-1999
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                                        CB390295 412 bp mRNA linear EST 15-WAY-2003
OSTE132B4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Marc vida@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:6239"
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| dev_stage="mixed stage"
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| dov_stage="mixed stage"
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| note="The AvrncDNA"
| note="The AvrncDNA"
| note | stages, embryos, adults and male N2 worms of subsequent generation of cDNAs by poly (A) priming. The cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GACTITITGCGGCGAGAAGGCGAAAGICTCAGTCGCTCTCCGAACTCCACGGAAACGTCTG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GAICTITGGAGCACGAAITCGAAIGAATCAGCAITCIGGGAGGGITCAAAACCITCIG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ332566
HS_5004_Al_F07_T7_RPCI11 Human Male BAC Library Homo sapiens
genomic_clone Plate=580 Col=13 Row=K, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression
Nat. Genet. (2003) In press
Contact. Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Farhd Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

    412
    70xganism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"

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GSS.
Homo sapiens (human)
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jWallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Splate: S80 row: K column: 13
Seq primer: T7
Class: BAC ends
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Mahairas, G.G., Wallace, T., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell type="Lymphocytes"
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/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GCGAAAGTCTCAGTCGCTCTCCGAACTCCACGGAAACGTCT 102
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=580 Col=13 Row=K"
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Location/Qualifiers
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complementary strand of a polymelectide which comprises a 5'-end sequence and an oligonuclectide which comprises a 5'-end sequence and an oligonuclectide comprises a 3'-end sequence complementary to a polymuclectide which comprises a 1'-end sequence complementary to a oligonuclectide comprises at 1'-end sequence complementary to a specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are also useful for the AAH13613 to AAH13613 to AAH13613 to AAH13613 to AAH13613 to AAH13613 and AAH13613 to AAH13613 to AAH13613 to AAH13613 and the present human amino acid sequences; and AAH13629 to AAH13612 represent concleoutides, all of which are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGGGGAGAAGGT
oligonucleotide comprising a sequence complementary to the
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                                                                                                                                                                                                                                                                                                                                                                                       23.2%; Score 30.6; DB 4; Length 567; 52.8%; Pred. No. 0.37;
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conditions, e.g. to the abolator, or years Arthory are incoming generate fusion proteins AABB1180-B51431. The genes can be used to generate fusion proteins by linking to the gene for the human common proteins by linking to the gene for the human conditions, e.g. by protein or gene therapy. The genes are isolated from conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the disgnosis, treatment and prevention of: (a) cancer, e.g. breast and cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allestgies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) canding anaemia allegates ampocardial ischemias; (d) wound healing canding and ulcerative colitis; (c) canding and protein as myocardial ischemias; (d) wound healing canding and ulcerative colitis; (d) canding
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                                                                                    The invention relate to the isolation of genes AAC93310-C93354 encoding
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                            Claim 1; Page 349; 410pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The invention relates to nucleic acid sequences (AAV84411 to AAV84633)

cocding human secreted proteins (AAW88534 to AAW886756). The secreted

protein gene sequences are deposited with the ATCC under deposit numbers

CC protein gene sequences are deposited with the ATCC under deposit numbers

CC 209011, 209080, 209081, 209083, 209084, 209085, 209009, 209010,

CO 209011, 209080, 209081, 209083, 209084, 209085, 209101,

CC sequences are used for the recombinant production of the secreted

CC sequences are used for the recombinant production of the secreted

CC proteins. The polynucleotide and animo acid sequences are useful for are

Useful for preventing, treating or ameliorating medical conditions e.g.

CC by protein or gene therapy. Pathological conditions can be also diagnosed

CC by determining the amount of the new polypeptides in a sample or by

CC determining the presence of mutations in the new polynucleotides, based on

CC specific uses are described for each of the polynucleotides, based on

CC specific uses are described for each of the polynucleotides, based on

CC specific uses are described for each of the polynucleotides, based on

CC specific uses are described for each of the polynucleotides, based on

CC disorders, developmental abnormalities and foortal deficiencies, blood

CC disorders, hepatic and renal disease of the immune system, autoimmune

CC disorders, prostate diseases, lymphomas, inflammation, allergies,

CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung

CC or thymus, diseasis, bendocine disorders, infections and AIDS. The

CD Dypeptides are also useful for identifying their binding partners. The

CD Dypeptides are also useful for identifying their binding partners. The

CN PROTEIN SECONAL STANDER AND SECONAL SECO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GAAAGTCTCAGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAT 123
Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C; Plorence K, Lafleur DW, Ni J, Pan P, Wei Y, Fischer CL, Soppet DR; Li Y, Zeng Z, Kyaw H, Yu G, Peng P, Dillon PJ, Endress GA; Carter KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
dermatological; immunosuppressive; antiinflammatory; immunostimulant;
cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                               WPI; 1999-059865/05.
P-PSDB; AAW88620, AAW88841, AAW88842, AAW88843, AAW88844, AAW88845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
23.2%; Score 30.6; DB 2; Length 1985;
Best Local Similarity 52.8%; Pred. No. 0.6;
Matches 66; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein gene 87 SEQ ID NO:97.
                                                                                                                                                                                                                            Claim 4; Page 347-348; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA83280 standard; cDNA; 1985 BP.
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                                                                                                                                 AAW88846.
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970S-0048995P.
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970S-0048997P.
970S-0048971P.
970S-0057644P.
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97US-005776P.
97US-0057771P.
97US-0057774P.
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97US-0057776P.
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97US-0070923P
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05-SEP-1997;
05-SEP-1997;
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                                                                                                                               06-JUN-1997
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05-SEP-1997
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05-SEP-19
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р, ; Hu

Rosen CA,

Ruben SM,

Ferrie AM,

Greene JM,

Young P,

neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;

124 ATTAC 128

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Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;
                                                                                                                                                                                         Claim 1; Page 968-969; 1533pp; English.
                                                                                  21-FEB-2001; 2001WO-US005614.
                                                                                           24-FEB-2000; 2000US-0184836P.
29-MAR-2000; 2000US-0193170P.
                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                          23.2%;
                                                                                                                                                                          preventing, diagnosing an and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                    66; Conservative
                                                                                                                                                                                                                                                                                                     the present invention
                                                                                                                                                     WPI; 2001-625724/72.
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                           P-PSDB; ABB50387
                                                             WO200162891-A2.
                                                    Homo sapiens.
                                                                        30-AUG-2001
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ACH0478
                                                                                                                                                                                                           proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in.

Example of these activities include: immunomodulatory; antisclerotic; dermacological; immunosupressive; antiinflammatory; immunostimulant; antipartimocnian; antimucorpial; antionvulsant; antialzheimers; vascular; antiparkimsonian; antimicrobial; and vulnerary. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease) (e.g. cancers and Changa's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy, neurological disorders (e.g. Huntington's chorea, and laser promoting wound healing, regeneration and/or chemotaxis. ABAB185 to the proposition of the exemplification of the proposition of the proposition of the exemplification of the coronary arteriors and the exemplification of the proposition of the exemplification of the coronary regions of the proposition of the exemplification of the coronary cancers and the proposition of the exemplification of the coronary cancers and the coronary regions of the proposition of the exemplification of the coronary cancers and the coronary regions of the exemplification of the coronary cancers and the coronary regions of the coronary cancers and the coronary regions of the coronary cancers and the coronary regions of the coronary cancers and parkingon's disease and parkingor regions of the coronary cancers and the coronary regions of the coronary cancers and parkingor regions of the coronary cancers and coronary regions of the corona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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Zeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA; Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y; Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Greene JM;
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Pred. No. 0.6;
0; Mismatches 59; Indels 0;
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Human, ss, gene therapy, autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telangiectasia; blood cagulation disorder; inflammatory condition; ischaemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection; ulcer; Alzheimer's disease; gene.
                                                                                                                                                                                           Novel human secreted protein #87 cDNA.
                                                                                    ACH04781 standard; cDNA; 1985 BP
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9705 0048884P
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9705 - 0048974P
9705 - 0049020P
9705 - 0049373P
9705 - 0049374P
9705 - 0049375P
9705 - 0055584P
9705 - 0055584P
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97US-0048881P.
97US-0048882P.
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97US-0048877P.
97US-0048878P.
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97US-0057634P.
97US-0057635P.
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                                                                                                                                                           (first entry)
1643 ATTTC 1647
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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06-JUN-1997;
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                                                                                                                                                         02-OCT-2003
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06-JUN-1997
                                                                                                                       ACH04781;
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The invention relates to an isolated HEMAEBO protein. The protein is useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple sclerosis and systemic lupus erythematosus; haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia telangiectasia; blood coagulation disorders e.g. afibrinogenaemia and thrombocytopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-reperfusion injury and arthritis; chyperproliferative disorders e.g. cancer and purpura; infectious disease e.g. viral infection and bacterial infection. The polymucleotide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzheimer's disease. The present sequence reperseents a novel human careful protein CDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at the content of the printed specification but was obtained in electronic condata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, Soppet DR;
Feng P, Dillon PJ, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young P, Greene JM, Ferrie AM, Olsen HS, Ebner R, Brewer LA, Florence K, Lafleur DW, Ni J, Li Y, Zeng Z, Kyaw H, Yu G, F Carter KC;
9705-0057643P.
9705-0057643P.
9705-0057648P.
9705-0057648P.
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9705-0057668P.
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P-PSDB; ABO44644.
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Human; ss; gene; secreted protein; precerebellin-like protein; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; mania; dementia; paranoia; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; hepatoblastoma; jaundice; hepatitis; immunological disorder; AlDS; leukaemia; rheumatoid arthritis; sepsis; acne; psoriasis; cancer.
                                                                      Human cDNA from novel secreted protein gene 87.
                                                                                                                                                                                                                                     970S-0048875P.
970S-0048878P.
970S-0048881P.
970S-0048881P.
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970S-004899P.
970S-004899P.
                ACD44591 standard; cDNA; 1985
                                                      (first entry)
                                                                                                                                                                                                                                                                           06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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06-JUN-1997;
06-JUN-1997;
                                                                                                                                                                  Homo sapiens
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                                                     10-SEP-2003
                                                                                                                                                                                                     25-FEB-2003
                                   ACD44591;
RESULT 6
ACD44591
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.; 0

Query Match
23.2%; Score 30.6; DB 8; Length 1985;
Best Local Similarity 52.8%; Pred. No. 0.6;
Matches 66; Conservative 0; Mismatches 59; Indels 0;

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CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT

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ATTTC 1647 124 ATTAC 128

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The invention relates to an isolated protein comprising amino acid residues 33-205 or 1-205 of a novel human secreted protein appearing as ABO26252. The protein sencoded by one of 238 disclosed CDNA sequences encoding 238 secreted proteins. ABO26252 is a precerbellin-like protein. Also included are a composition comprising the protein and a carrier and an isolated protein produced by expressing the protein and a carrier and or isolated protein produced by expressing the protein cited above by a cell, and recovering the protein. The proteins are useful for diagnosing or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, Schizophrenia, mania, dementia, paranoia, psychoses or autism), immune disorders (e.g. hepatchlastoma, jaundice, hepattitis), immunological disorders (e.g. AIDS, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wal Y, Fischer CL, Soppet DR;
Feng P, Dillon PJ, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New precerebellin-like protein, useful for diagnosing or treating neurodegenerative and behavioral disorders, immune disorders, liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 97; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Greene JM, Ferrie .... S, Ebner R, Brewer LA, 1:e K, Lafleur DW, Ni J, 1:e K, 7 Kvaw H, Yu G, F
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97US-0057654P.
97US-0057661P.
97US-0057662P.
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9705-0057762P
9705-0057763P
9705-0057764P
9705-0057768P
9705-0057770P
                                            970S-0049375P.
970S-0057584P.
970S-0057627P.
970S-0057628P.
970S-0057629P.
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970S-0057646P.
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970S-0057648P.
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97US-0057666P.
97US-0057667P.
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97US-0057775P.
97US-0057776P.
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97US-0057778P.
97US-0070923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young P, Greene JM,
Olsen HS, Ebner R, B
Florence K, Lafleur D'
Li Y, Zeng Z, Kyaw H
Carter KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, and cancer.
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06-dUN-1997;
06-dUN-1997;
05-SEP-1997;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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05-SEP-1997;
18-DEC-1997;
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rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present sequence is one of the 238 disclosed cDMAs encoding a novel secreted protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at:- seqdata.uspto.gov/sequence.html?DocID=6525174B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                    63
                                                                                                                                                                                                                 cerreacreceágeacerracecaacagaraagergaarececerreacerrergarar
                                                                                                                                                                                                                                               64 GAAAGICICAGITTICCGAACTCCACGIAAACGIGTGCTCCTAAGACGCAAACAAT
                                                                                                                                                                                    4 CCTTGTCTACTACTCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                     .
0
                                                                                                                        Score 30.6; DB 8; Length 1985; Pred. No. 0.6;
                                                                                           Sequence 1985 BP; 467 A; 542 C; 466 G; 506 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 115; 2081pp + Sequence Listing; English.
                                                                                                                                                       59; Indels
                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 115.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABL89553 standard; cDNA; 1987 BP.
                                                                                                                      23.28;
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                                                                                                                                                        66; Conservative
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                                                                                                                                                                                                                                                                                                                                      1643 ATTTC 1647
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                           124 ATTAC 128
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Best Local S
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

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1587 disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaema, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and paraëltic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 1588 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTTCCAAAATGGCCTTTATC 1647 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 63 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. 1528 cchicacheceaecaccheceaecaeanaaeanaacheeareeccheecenereaana 64 GARAGICICAGICGCITICCGAACTCCACGIAAACGIGTGCTCCTAAGACGGCAAACAAT 4 CCTTGTCTACTACTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 0; Gaps Yamamoto Match
Local Similarity 52.8%; Pred. No. 0.6;
es 66; Conservative 0; Mismatches 59; Indels 0; Claim 8; SEQ ID NO 12295; 2537pp + Sequence Listing; English. Sequence 1987 BP; 464 A; 548 C; 467 G; 507 T; 0 U; 1 Other; Isogai T, Nishikawa T, Hayashi K, Saito K, Sugiyama T, Wakamatsu A, Nagai K, Otsuki Human cDNA sequence SEQ ID NO:12295. AAH14641 standard; cDNA; 2510 29-JUL-1999; 99JP-00248036. 27-ANG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-NAX-2000; 2000JP-00183767. 28-JUL-2000; 2000EP-00116126 (first entry) (HELI-) HELIX RES INST WPI; 2001-318749/34. 1648 ATTTC 1652 124 ATTAC 128 EP1074617-A2. Homo sapiens 26-JUN-2001 07-FEB-2001 Ś AAH14641; Query Match Ota T, Ishii S ø a 8888888888888 원 ð ò ò 엄

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nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end sequence and an oligonucleotide which comprises a 3'-end sequence complementary to a complementary strand of a polynucleotide which comprises a 3'-end sequence, where the combination of oligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the comprises and the grainer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in comprises the remaining of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs casily without any specialised methods. AdMO3166 to AdM13628 and AdM13633 reparesent human amino acid sequences; and AdM13632 reparesent consideration of the consideration of the complexities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGCCAAACAAT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 23.2%; Score 30.6; DB 4; Length 2510; Local Similarity 52.8%; Pred. No. 0.66; hes 66; Conservative 0; Mismatches 59; .Indels 0.
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AA160107/c
ID AA160107 standard; CDNA; 2793 BP.
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200UUS-00582117.
200UUS-00582017.
200UUS-0059042.
200UUS-00620312.
200UUS-00653450.
200UUS-0065191.
200UUS-0065191.
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25-APR-2000; 2
20-JUN-2000; 2
19-JUL-2000; 2
13-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
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Matches
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WO200157182-A2
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                                                                                     Matsuda A,
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                                                                                                                                                                    The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM8642-AAM4213) with nootropic, immunosuppersant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system classes, such as localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic localised neuropathies and central nervous system suppression, at alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosasis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                        Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerreacreceadeacerreceaacadaraacregareceerregeerrergaarar 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                           el nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGGCGAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease; cancer; infectious disease; bone disease; AIDS; neurodegenerative disease; ischaemic disorder; Antiinflammatory; Immunoedulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV; Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
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0
                        Ren F,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                Length 2793;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 2793 BP; 686 A; 707 C; 743 G; 653 T; 0 U; 4 Other;
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                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                Score 30.6; DB 4;
Pred. No. 0.69;
                        Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                Claim 1; SEQ ID NO 4096; 10078pp; English.
                       ndi V, Chen R,
rman T, Xu C,
Drmanac RT;
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                    Liu C, Asundi V,
Wang Z, Wehrman T,
Goodrich R, Drmanac
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52.8%;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.8'
                                                                      WPI; 2001-442253/47
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(HYSE-) HYSEQ INC
                                                                                     P-PSDB; AAM40951
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                                   Wang J,
Zhou P,
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                                                                                                            Novel
                        Tang
Wang
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ADC37174
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2499 cccaererereageirreccaagaccacrerecereregecreecaaaregecrerate 2558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified protein that activates nuclear factor kappa B (NF-kappaB),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2439 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGCCTTCTGAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2867 BP; 662 A; 761 C; 747 G; 697 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 7; 938pp; English.
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03-DEC-2001; 2001JP-00368692.
05-DEC-2001; 2001JP-0038829P.
03-OCT-2002; 2002JP-00291302.
04-OCT-2002; 2002US-0415769P.
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16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
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24-FEB-2000; 2000US-0184664P.
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                                                                                                                                                                                                                                                                                                                           WPI; 2003-505282/47.
                                                                                                                                                                              (ASAH ) ASAHI KASEI
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63

2000US - 0205515P.
2000US - 0214886P.
2000US - 0214886P.
2000US - 0214886P.
2000US - 0217489P.
2000US - 0217489P.
2000US - 021898P.
2000US - 0225213P.
2000US - 0231414P.
2000US - 02314 19-WAY-2000, 201-44-2000, 201-44-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-444-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-44-2000, 201-42-20

20-CCT-2000; 2000US-0241221P.
20-CCT-2000; 2000US-0241785P.
20-CCT-2000; 2000US-0241787P.
20-CCT-2000; 2000US-024180F.
20-CCT-2000; 2000US-0241809P.
20-CCT-2000; 2000US-0241809P.
20-CCT-2000; 2000US-0241809P.
20-CCT-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024921P.
08-NOV-2000; 200US-024921P.
08-NOV-2000; 200US-

Listing; English Disclosure; SEQ ID NO 40447; 3071pp + Sequence

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

ΣS

Ruben

Barash SC, GENOME

Rosen CA, (HUMA-)

HUMAN

WPI; 2001-483426/52

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM81170 to AAV31921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleorides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For

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2000US-0225270P.
2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
2000US-0225758P.
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                                                                                                                                                                                                                                                      23-AUG-2000) 2000US-022.02
30-AUG-2000) 2000US-0228924P.
01-SEP-2000; 2000US-0229287P.
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2000US-0235836P.
2000US-0236327P.
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29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-0CT-2000; 2000US-0236802P.
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2000US-0236368P.
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2000US-0237039P.
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     21165 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGCCTTCTGAATAT 21224
                                                                                                                                                                                                                                                                                                                                              21225 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTCCAAAATGGCCTTTATC 21284
example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK45492 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                    64 GAAAGTCTCAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; dimunosuppressive; antihiflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antifreumatic; hepatotropic; crebroprotective; antiinflammatory; antiallergic, antidiabetic; antiuler; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                               4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 Sequence 22013 BP; 5294 A; 5048 C; 5035 G; 6636 T; 0 U; 0 Other;
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0
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Pred. No. 1.5;
0; Mismatches 59; Indels 0;
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02-MAR-2000; 2000US-0189550P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0199076P.
18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205515P.
07-UN-2000; 2000US-0209467P.
28-UUN-2000; 2000US-0218486P.
30-UUN-2000; 2000US-0214886P.
                                                                                                                                                                                                          ch 23.2%;
1 Similarity 52.8%;
66; Conservative
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04-FEB-2000; 2000US-0180628P
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                                                                                                                                                                                                                         Local Similarity
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ABA16084
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2000US-0249211P
2000US-0249213P
2000US-0249215P
2000US-0249215P
2000US-0249215P
2000US-0249218P
2000US-0249218P
2000US-0249248P
2000US-0249244P
                                                                                                                                                              2000US-0246526P

2000US-0246527P

2000US-0246532P

2000US-0246610P

2000US-0246610P

2000US-0246611P

2000US-0246611P

2000US-0246611P

2000US-0246611P

2000US-0246611P

2000US-0249201P

2000US-0249203P

2000US-0249203P
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2000US-0249297P.
2000US-0249299P.
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2000US-0250391P.
2000US-0251160P.
08-NOV-2000; 208-NOV-2000; 208
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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Tue Oct 12 09:20:48 2004

05-JAN-2001; 2001US-0259678P

2000US-0251479P-2000US-0251856P-2000US-0251868P-2000US-0251869P-2000US-0251990P-2000US-0251990P-

2000US-0251030P. 2000US-0251988P. 2000US-0256719P.

Ruben SM Rosen CA, Barash SC,

WPI; 2001-541565/60

3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system cancers Nucleic acids encoding useful for preventing, and metastases.

Disclosure; SEQ ID NO 8415; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing

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21224
                                                                                                                                                                                                                                                                 21225 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCCTGTGGGCTTCCAAAATGGCCTTTATC 21284
; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                 64 GAAAGICTCAGGTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                    4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                            Seguence 22013 BP; 5294 A; 5048 C; 5035 G; 6636 T; 0 U; 0 Other;
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                                                                                                                           5; Length 22013;
                                                                                                                                                        59; Indels
                                                                                                                        Query Match
23.2%; Score 30.6; DB
Best Local Similarity 52.8%; Pred. No. 1.5;
Matches 66; Conservative 0; Mismatches
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24-FEB-2000; 2000US-0186464P.
02-MAR-2000; 2000US-0186464P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0188914P.
17-MAR-2000; 2000US-0198174P.
18-MAR-2000; 2000US-0198174P.
19-MAY-2000; 2000US-0198174P.
19-MAY-2000; 2000US-0198174P.
10-JUL-2000; 2000US-0214886P.
10-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-021488P.
11-JUL-2000; 2000US-021488P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02148P.
11-JUL-2000; 2000US-02148P.
14-JUL-2000; 2000US-02214P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225268P.
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AAK85636
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0) 2000US-0229343P. 0) 2000US-0229344P. 0) 2000US-0229345P. 0) 2000US-0229509P. 0) 2000US-0229513P.

01-SEP-2000; 2 01-SEP-2000; 2 01-SEP-2000; 2

05-SEP-2000; 2 05-SEP-2000; 2 06-SEP-2000; 2 06-SEP-2000; 2

08-SEP-2000; 208-SEP-2000; 208

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

08-SEP-2000 -SEP-2000

-SEP-2000

23-AUG-2000; 2000US-02270099. 30-AUG-2000; 2000US-0228924P. 01-SEP-2000; 2000US-0229287P.

2000US-0246474P 2000US-0246475P. 2000US-0246476P. 2000US-0246477P. 2000US-0246478P.

38-NOV-2000;

38-NOV-2000;

08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

2000US-0237039P. 2000US-0237040P. 2000US-0239935P. 2000US-0239937P. 2000US-0240960P.

02-OCT-2000; 02-OCT-2000; 13-OCT-2000;

13-OCT-2000 20-OCT-2000

2000US-0241221P. 2000US-0241785P. 000US-0241786P 2000US-0241787P. 2000US-0241809P 2000US-0241826P. 2000US-0244617P.

20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000;

2000US-0237038P

32-OCT-2000

2000US-0236369P. 000US-0236802P.

29-SEP-2000 29-SEP-2000

2000US-023636BP

27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

25-SEP-2000

26-SEP-2000

21-SEP-2000

.4-SEP-2000 21-SEP-2000

4 CCTIGICIACIAGICCCTIACCGAGIAAGGAAAIGIACCGGACTITIGCGGCGAGAGGI 63 Gaps Sequence 22026 BP, 5289 A; 5044 C; 5030 G; 6663 T; 0 U; 0 Other; . 0 Query Match
23.2%; Score 30.6; DB 4; Length 22026;
Best Local Similarity 52.8%; Pred. No. 1.5;
Matches 66; Conservative 0; Mismatches 59; Indels 0;

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and sequences given in AAM81170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I). by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to protein. (I) additionally cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artisen genomic cancers and capresent human immune/haematopoietic artisen genomic sequences from the present invention. AAK54930 and AAM82169 represent invention. Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. Disclosure; SEQ ID NO 40448; 3071pp + Sequence Listing; English. Barash SC, Ruben SM; 2000US-0246611P. 2000US-0246613P. 2000US-0249207P. 2000US-0249215P. 2000US-0249216P. 2000US-0249217P. 2000US-0249208P 2000US-0249209P 2000US-0249211P. 2000US-0249210P 2000US-0249213P 2000US-0249218P 2000US-0249264P 2000US-0249299P 2000US-0249300P 000US-0249214P 2000US-0249244P 2000US-0249265P 2000US-0249297P 2000US-0250160P 2000US-0251030P 2001US-0259678P (HUMA-) HUMAN GENOME SCI INC WPI; 2001-483426/52 08-NOV-2000; 2 17-NOV-2000; 2 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 17-NOV-2000; 11-DEC-2000; 05-JAN-2001; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 08-DEC-2000; **38-DEC-2000** Rosen CA,

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21178 CCTTCACTCCCAGCACCTTGCCCAACAGGATAAGCTGGATCCCCTTGGACTTCTGAATAT 21237
                                                                          21238 CCCAGTGTCTTCAGGTTTCCCAAGACCACTTCCTGTGGGCTTTCCAAAATGGCCTTTATC 21297
                                               GAAAGICICAGTCGCTTTCCGAACTCCACGTAAACGTGTGCTCCTAAGACGGCAAACAAT 123
                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antisherdic; antidabetic; errebroprotective; antiinflammatory; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                     Human nervous system related polynucleotide SEQ ID NO 8416.
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24-FEB-2000; 2000US-0186464P.
22-MAR-2000; 2000US-0186464P.
02-MAR-2000; 2000US-0186350P.
15-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0199874P.
18-MAR-2000; 2000US-0199874P.
19-MAY-2000; 2000US-0199874P.
19-MAY-2000; 2000US-0199874P.
19-MAY-2000; 2000US-019880P.
19-MAY-2000; 2000US-021488P.
11-JUL-2000; 2000US-021488P.
11-JUL-2000; 2000US-021487P.
11-JUL-2000; 2000US-021487P.
11-JUL-2000; 2000US-021835P.
26-JUL-2000; 2000US-02183P.
14-MUG-2000; 2000US-02181P.
14-MUG-2000; 2000US-02251P.
14-MUG-2000; 2000US-02251P.
14-MUG-2000; 2000US-022526FP.
14-MUG-2000; 2000US-02252FP.
14-MUG-2000; 2000US-02252FP.
14-MUG-2000; 2000US-02252FP.
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17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
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17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249309P.
01-DEC-2000; 2000US-0250391P.
01-DEC-2000; 2000US-0251050P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025103P.
06-DEC-2000; 2000US-0251479P.
06-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
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05-JAN-2001; 2001US-0259678P
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viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriabais; rheumatoid arthritis; aterila inflammatory atthms; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                   Human cDNA differentially expressed in granulocytic cells #142.
                                                                                                                                      granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                  Vockley J;
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                                                                                                                                                                                                                                                                                                                                  Weissman SM, Yamaga
                                                              ABK83571 standard; cDNA; 175737 BP.
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                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
                21298 ATTTC 21302
124 ATTAC 128
                                                                                                                                                                                                                                                                                                                                  Beazer-Barclay Y,
                                                                                                                                                                                                                                        WO200228999-A2
                                                                                                  14-AUG-2002
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                                                                                 ABK83571;
                                                      ABK83571
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gaiven in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are condulating (M2) GAA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a cissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression of crissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene (S) from GS, where the level of expression in a sample of the tissue of gene (S) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by conteacting a tissue having inflammation with an agent that modulates the expression of gene(S) from GS, M3 is useful for detecting an inflammation in a tissue, M4 is useful for modulating GA, M3 is useful for exposure of a subject to a pathogen or sterile inflammation in a tissue, M4 is useful for detecting an inflammation in a tissue, M4 is useful for modulating GA, preferably in an inflammation in a tissue, M4 is useful for detecting an inflammation (especially chronic) in a tissue, an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, senal reperfusion injury, senal reperfusion injury, senal reperfusion injury, senal reperfusion injury, s Claim 1; SEQ ID NO 142; 114pp; English.

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4 CCTTGTCTACTAGTCCCTTACCGAGTAAGGAAATGTACCGGACTTTTGCGGCGAGAAGGT 63

Query Match 23.2%; Score 30.6; DB 5; Length 22026; Best Local Similarity 52.8%; Pred. No. 1.5; Matches 66; Conservative 0; Mismatches 59; Indels 0;

; 0

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic genes associated with granulocyte activation, which serves as diagnostion markers that is useful for monitoring disease states and drug toxicity.

WPI; 2002-435328/46.

us-10-009-317a-30.rng

Search completed: October 11, 2004, 09:30:38 Job time : 194 secs

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Sequence 49, Appl
Sequence 41896, A
                                                                              October 26, 2004, 15:20:02; Search time 31.5 Seconds (without alignments) 37.896 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-309-487-9
US-09-917-3487-9
US-10-141-645-1
US-09-917-340-53
US-10-141-645-4
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US-10-141-645-9
US-09-967-808-21
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US-09-309-487-214
US-09-309-487-214
US-09-309-487-218
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US-09-309-487-286
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Vuan, Jun
APPLICANT: Outlette, Jun
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPREBENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
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US-08-630-915A-37
US-09-879-957-37
US-09-252-951A-32502
US-09-252-991A-32312
US-09-086-445-30
US-07-966-349A-6
US-09-664-864-9
US-10-642-872-9
US-10-642-872-9
US-10-642-872-9
US-09-637-650B-5
US-09-637-650B-1
US-09-637-650B-1
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US-09-637-650B-1
US-09-637-650B-1
US-09-436-063C-7
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Patent No. 6335318
GENERAL INFORMATION:
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US-09-309-487-1
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US-09-309-487-1
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80.2%;
ORGANISM: Artificial Sequence
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                                                                                        Query Match
Best Local Similarity 77.8%
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; ORGANISM: Macaca mulatta
US-09-967-808-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type: PRT CAGANISM: Macaca mulatta US-09-309-487-9
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US-09-309-487-9
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                                                                                 Query Match 87.1%; Score 101; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 1.3e-05; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.2%; Score 93; DB 4; Length 18; Best Local Similarity 77.8%; Pred. No. 0.0001; Matches 14; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     US-10-141-645-5

US-10-141-645-5

Sequence No. 6713078

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alaxander Cole

APPLICANT: Alaxander Cole

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Retrocyclins - Antiviral

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT APPLICATION NUMBER: 602-06

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO SEQ ID NOS: 125

LESCHARE: FastSEQ for Windows Version 4.0

LEGGTH: 18
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GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PASSES for Windows Version 4.0
SEQ ID NO 5
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic variant US-10-141-645-5
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; TYPE: PRT; ORGANISM: Macaca mulatta
US-09-967-808-1
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APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Xi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Van, Jun
APPLICANT: Outlette, Jun
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFRENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT PILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 18
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| Sequence 9, Application US/09967808
| Patent No. 514427.
| GENERAL INFORMATION:
| APPLICANT: Tang, Yi.Quan
| TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
| TITLE OF INVENTION: Andre J.
| TITLE OF INVENTION WIMBER: US/09/967,808
| CURRENT FILING DATE: 2001-09-26
| PRIOR FILING DATE: 1999-05-10
| NUMBER OF SEQ ID NOS: 31
| SOFTWARR: Patentin Ver. 2.0
| SEQ ID NO 9-
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Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 2; Indels
                                                                                                            Score 93; DB 4; Length 18;
Pred. No. 0.0001;
1; Mismatches 3; Indels
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Best Local Similarity 81.2%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                   1; Mismatches
FEATURE:
, OTHER INFORMATION: synthetic variant
US-10-141-645-6
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09309487; Patent No. 6335318; GENERAL INFORMATION:
                                                                                                                                                                                                                            1 GFCRCICTRGFCRCICTR 18
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Query Match 75.0%; Score 87; DB 4; Length 18; Best Local Similarity 72.2%; Pred. No. 0.00047; Matches 13; Conservative 1; Mismatches 4; Indels
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; Sequence 3, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
    APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Alexander Cole
; APPLICANT: Alexander Cole
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: 06/284,855
; PRIOR PILLING DATE: 2002-04-18
; PRIOR PILLING DATE: 2002-04-18
; PRIOR PILLING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO
; LEMORTH: 18
                                      APPLICANT: ACBET LETREE

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retricyclins - Antiviral and
TITLE OF INVENTION: Actimicrobial Peptides

FILE REFERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: 105/10/141,645

CURRENT APPLICATION NUMBER: 60/284,855

PRIOR PILING DATE: 2001-04-18

PRIOR PILING DATE: 2001-04-18

PRIOR PILING DATE: 2002-06-18

PRIOR PILING DATE: 2002-06-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO S: 125

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Robert Lehrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-141-645-3
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                                                                          APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE REPERENCE: UCLA-001CIP;
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: US/10/141,645
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE FRAESEQ for Windows Version 4.0
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Sequence 53, Application US/09917340

Patent No. 669228

GENERAL INCREMETON:
APPLICANT: Murphy, Christopher J.
APPLICANT: Machaulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT PELLICATION NUMBER: US/99/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR PELLING DATE: 2000-07-28
PRIOR FILING DATE: 2000-117
PRIOR FILING DATE: 2000-117
PRIOR FILING DATE: 2000-117
PRIOR FILING DATE: 2001-07-3
PRIOR FILING DATE: 2001-07-3

REIGN FILING DATE: 2001-07-3

FRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 53

LENGTH: 18
                          Sequence 1, Application US/10141645 Patent No. 6713078
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; ORGANISM: Macaca mulatta
US-09-917-340-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Homo sapiens
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Matches 14, Conserv
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Score 75; DB 4; Length 18; Pred. No. 0.01; 0; Mismatches 6; Indels
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64.7%; Score 75; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 6; Indels
                     Sequence 8, Application US/10141645
; Sequence 8, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alan Waring
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT PAPLICATION NUMBER: US/10/141,645
; CURRENT PILING DATE: 2002-05-06
; PRIOR FILING DATE: 2001-04-18
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
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JOS-102-10-10-15-5

JOS-102-10-15-5

JOS-102-10-15-5

JOS-102-10-15-5

JOS-102-10-15-5

JOS-102-15-5

JOS-102-16-18

JOS-102-16-18

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFCRCICTRGFCRCICTR 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.7%;
Best Local Similarity 66.7%;
Matches 12; Conservative
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ORGANISM: Artificial Sequence
               US-10-141-645-8
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71.6%; Score 83; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 5; Indels
US-1U-141-045-94
) Sequence 4, Application US/10141645
) Patent No. 6713078
) GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alaxander Cole
APPLICANT: Alaxander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UGLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
FRIOR PELING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS: 125
ILENGTH: 18
ILENGTH: 18
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Patent No. 6713078

GENERAL INFORMATION:
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alaxander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT PILICATION NUMBER: US/10/141,645
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: Unssigned
PRIOR APPLICATION NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: synthetic variant US-10-141-645-4
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; OTHER INFORMATION: synthetic variant
US-10-141-645-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFCRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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1; Mismatches
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 83.3%;
Matches 10; Conservative
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CRGANISM: Macaca mulatta
US-09-309-487-14
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US-09-309-487-29
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US-09-309-487-29
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                                                                     RESULT 15
US-09-300-487-21
Sequence 21, Application US/09309487
Patent No. 633518
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Vuan, Jun
APPLICANT: Outlette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPRENCE: P-UC 3095
CURRENT APPLICANTION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 21
LENGTH 92
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Fatent No. 6514727

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Yean, Jun

APPLICANT: Yean, Jun

APPLICANT: Yean, Jun

TITLE OF INVENTION: Same

FILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/967,808

CURRENT APPLICATION NUMBER: US/09/967,808

FRIOR PILLORATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31-05-10

SOFTWARE: PATENTIN OF: 2.0

SEQ ID NO 21

LENGTH: 92

MANDER OF SEQ ID NOS: 31-05-10

SEQ ID NO 21

LENGTH: 92
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Pred. No. 0.062;
1; Mismatches 1; Indels
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Pred. No. 0.062;
1; Mismatches 1; Indels
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Patent No. 6335318
GENERAL INFORMATION:
APPLICANT: Seleted, Michael E.
1 GICICGRGICYCICGR 18
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84.6%;
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6
Matches ,11; Conservative
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; ORGANISM: Macaca mulatta
US-09-309-487-21
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US-09-967-808-21
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RESULT 17

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Sequence 29, Application US/09309487

Sequence 29, Application US/09309487

Sequence 29, Application US/09309487

Settle No. 6335318

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Septent No. 6335318

Septent No. 6335318

APPLICANT: Selsted, Michael E.

APPLICANT: Youn, Jun

APPLICANT: Youn, Jun

APPLICANT: William Jun

SEPTING OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: P-VO. 2095

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 76

LENGTH: 76
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APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Yun
APPLICANT: Vun, Jun
APPLICANT: Ouellette, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFRENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 76
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Patent No. 6514727

GENERAL INFORMATION

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan.

APPLICANT: Tang, Yi-Quan.

APPLICANT: Tang, Yi-Quan.

APPLICANT: Vaun, Jun

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using

TITLE OF INVENTION: Same

FILE REPERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/967,808

CURRENT FILING DATE: 2001-09-26

PRIOR PELING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 14
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Pred. No. 0.54;
1; Mismatches 1; Indels
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Pred. No. 0.54;
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Gaps
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KLEIN, BARBARA K
MCWHERTER, CHARLES A
STATEN, NICHOLAS R
STUMERS, NEENA L
BAUDER, S C
LEE, STEPHEN C
LIEE, STEPHEN C
AGONISTS
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                                                  Score 64; DB 4; Length 76; Pred. No. 0.54; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNIS A. BENNETT, G.D. SEARLE & CO.,
CORPORATE PATENT DEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-200
CLASSIFICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-200
CLASSIFICATION: vUnknown-
PRIOR APPLICATION NUMBER: W0 PCT/US 96/15774
APPLICATION NUMBER: US 60/004,834
FILING DATE: 05-CCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENNETT, DENNIS A
REFERENCE/DOCKET NUMBER: 34,547
REDESCROMUNICATION NUMBER: 34,547
TELECOMMUNICATION NUMBER: 34,547
TELECOMMUNICATION NUMBER: 210/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 286: US-09-510-238A-286
                                                                                                                                                                                                                                                                                   Sequence 286, Application US/09510238A Patent No. 6730303 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHRACTERISTICS:
LENGHT: 180 amino acid
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 314-694-5402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. BOX 5110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               CAPARON, MAIRE H
ZURFLUH, LINDA L
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FENG, YIQING BAUM, CHARLES M
                                                        Query Match 55.2%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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Best Local Similarity
Matches 9; Conserva
; LOCATION: (1)...(20) US-10-141-645-15
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Sequence 29, Application US/09967808.

Senent No. 6514727.

GENERAL INFORMATION:

APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANTON WHERE: US/09/967,808
CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 76
                                                                                                                                                    Gaps
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0.54;
                                                                                                      Score 64; DB 4; Length 76;
Pred. No. 0.54;
1; Mismatches 1; Indels
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
ITLE OF INVENTION: Retrocyclins - Antiviral and
ITLE OF INVENTION: Antimicrobial Peptides
ITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOTTWARE: 76
LENGTH: 76
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Pred. No. 0.54;
1; Mismatches
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Patent No. 6713078
GENERAL INFORMATION:
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83.3%;
                                                                                                             55.2%;
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Best Local Similarity 83.3
The Local Similarity 83.3
                                                                                                      Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                4 RCICTRGFCRCI 15
                                                                                                                                                                                                                               65 RCICTRGFCRLL 76
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ORGANISM: Macaca mulatta
                              ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-967-808-29
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NAME/KEY: SIGNAL
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US-09-967-808-29
             LENGTH: 76
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4 RCICTRGFC 12
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US-003-309-487-18
US-003-309-487-18
Sequence 18, Application US/09309487
Sequence 18, Application US/09309487
SEQUENCE SELECT TO SET SELECT SELECT SELECT SELECT SELECT SELECT SELECT SERVER. Trang. Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Ovellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPREBRENCE: PUG 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
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US-09-967-808-18
i Sequence 18, Application US/09967808
j Patent No. 6514727
i GENERAL INFORMATION:
j APPLICANT: Selsted, Michael E.
j APPLICANT: Selsted, Michael E.
j APPLICANT: Tang, Yi-Quan
j APPLICANT: Yuan, Jun
j APPLICANT: Ovellette, Andre J:
j TITLE OF INVENTION: Same
j TITLE OF INVENTION NUMBER: US/09/967,808
j CURRENT FILING DATE: 1999-05-10
j NUMBER OF SEQ ID NOS: 31
j SOFTWARE: PatentIN Ver. 2.0
j SEQ ID NO 18
j LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.0%; Score 58; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-141-645-36
'Sequence 36, Application US/10141645
'Retent No. 6713078
1 GFCRCICTRGFCRCIC 16
                                               8 cacccacrrcccrcrc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RCICTRGFC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9
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Matches
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APPLICANT. Robert Labers
APPLICANT. Alam Wating
TITLE OF INVESTION: Retrocyclis.
APPLICANT. Peress And Order
TITLE OF INVESTION: Retrocyclis.
APPLICANT. ON The Residence Cold.
APPLICANT. Peress And Order
TITLE OF INVESTION: Retrocyclis.
APPLICANT. Roberts. 2002-06-16
CURRENT PROFICATION NUMBER: Unsesigned
PROR FILING DATE. 2002-06-16
PROR PRICALING DATE. 2002-06-16
PROR PRICALING DATE. 2002-06-16
PROR PRICALING DATE. 2002-06-16
PROR PRICALING DATE. 2002-06-16
PROPER INVESTION NUMBER: Unsesigned
PROR FILING DATE. 2002-06-16
PROPER INVESTION SEQUENCE OF Mindows Version 4.0
SUBJECT OF SEQUENCE AND SEGUENCE OF MANAGEMENT ROBERT LORD SEGUENCE OF MANAGEMENT AND SEGUENCE OF MANAGEMENT ROBERT LORD SEGUENCE OF MANAGEMENT AND SEGUENCE OF M
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Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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US-09-252-991A-32502
                   US-08-630-915A-37
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US-09-270-767-41896

Sequence 41896, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NOWHER OF SEQ ID NOS: 62517

SEQ ID NO 41886

LENGTH: 323

LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08630915A

Patent No. 630920

GENERAL INFORMATION:
APPLICANT: SPAKES, Andrew B.
APPLICANT: FOWLKES, Dana M.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 4; Length 323;
Pred. No. 13;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PTLING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Pennie & Edmonds LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 FCKSYCTFFCRLFCAR 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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US-08-630-915A-37
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APPLICANT: SPARKS, Andrew B.
HOFFRAN, No. 6709821h
KAY, Brian K.
KAY, Brian K.
MCCONNELL, Dana M.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                               Gaps
                                               1;
47.8%; Score 55.5; DB 3; Length 1400; 58.8%; Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELESPACE: (212) 866-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-JUN-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-879-957-37
                                                                                                                                                                                                                                                Sequence 37, Application US/09879957
Patent No. 6709821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66.41 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
TYPE: amino acid
                                                                                                                                   117 égéaccéredre-caér 132
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                                                                                          1 GFCRCICTRGFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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US-07-906-349A-6
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Sequence 3221, Application US/0925291A

Referent No. 6551795

Referent No. 6551795

Referent No. 6551795

Referent No. 6551795

TILLS OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

TILLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PRILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 585

TYRE: PRT

CREAMISM: PSECULATION NUMBER: US 60/094,190

REGION OF SEQ ID NOS: 33142

CREAMISM: PSECULATION NUMBER: US 60/094,190

ROGANISM: PSECULATION NUMBER: US 60/094,190
Sequence 32502, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SELING DATE: 1998-02-18
PRIOR SELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Patent No. 6703485

Patent No. 6703485

APPLICANT: Kandel, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Bartsch, Dusan
APPLICANT: Sleeshbaum, Steven
APPLICANT: Grant, Seth
APPLICANT: Grant, Seth
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
47.4%; Score 55; DB 4; Length 168;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32502
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150 CRCSRGPCRCACS 162
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US-09-086-436-30
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APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: A ROYEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS
NUMBER OF SEQUENCES: 16
CORRESSONERCES: 16
CORRESSONERCES: 16
CORRESSONERCES: 16
CORRESSONERCES: 16
COUNTRY: USA
STREET: 419 Seventh Street, N.W.
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: ZOOO,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349A
FILING DATE: 30-JUN-1991
CLASSIFICATION NUMBER: US/07/906,349A
FILING DATE: 18-JAN-1991
TELECOMMUTCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                    47.4%; Score 55; DB 4; Length 2732;
57.1%; Pred. No. 90;
tive 0; Mismatches 6; Indels
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Pred. No. 39;
0; Mismatches
FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: U3/09/086,436
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 30
LENGTH: 2732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/07906349A Patent No. 5434064 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 GTCACCCTGTGACCCTCT 362
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative (
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Best Local Similarity 57.14
Best Local 8; Conservative
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, MOLECULE TYPE: protein
US-07-906-349A-6
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STRANDEDNESS: si
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Murine
US-09-086-436-30
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Query Match
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                                                        APPLICANT: Hancock, Robert E. W.
APPLICANT: Along, Lijuan
TITLE OF INVENTION: WITHEROFF PEPTIDES AND METHODS OF
TITLE OF INVENTION: UST THEREOFF
FILE REFERENCE: UBC1170
CURRENT APPLICATION NUMBER: US/09/604,864
CURRENT FILING ANTE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 3; Length 18; Pred. No. 2.4; 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
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Sequence 8, Application US/10042872
Batent No. 6747007
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: Hancock, Robert B. W.
APPLICANT: Zhang, Lijuan
ITILE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
Sequence 8, Application US/09604864
Patent No. 6337317
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-09-604-864-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FCRCICTRGFCRCIC 16
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                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
US-09-604-864-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Sequence 5, Application US/09627650B;
Patent No. 640681A:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Methods Related Thereto
FILE PEPERENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
FRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
SPRIOR FILING DATE: 1998-11-09
SOFTWARE: PATENTING DATE: 1998-11-09
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                                                                                                                                                                                                              Score 54; DB 4; Length 18; Pred. No. 2.4;
                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA

APPLICANT: HANGOCK, ROBERT E. W.

APPLICANT: HANGOCK, ROBERT E. W.

APPLICANT: ANTIMICROBIAL PEPTIDES AND METHODS OF

TITLE OF INVENTION: USE THEREOF

FILE REPERRICE: UBC1.70-1

CURRENT APPLICATION NUMBER: US/10/042,872

CURRENT APPLICATION NUMBER: US/20/2-01-08

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-042-872-9; Sequence 9, Application US/10042872; Patent No. 6747007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Caenorhabditis elegans US-09-627-650B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%;
                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                          ; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-10-042-872-8
                                                                                                                                                                                                                                                                                                                              2 FCRCICTRGFCRCIC 16
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ORGANISM: Limulus polyphemus
US-10-042-872-9
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Best Local Similarity 60.03
Matches 9; Conservative
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US-09-627-650B-5
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Job time : 31.5 secs
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US-09-436-063C-5
Sequence 5. Application US/09436063C
Sequence 5. Application US/09436063C
Sequence 5. Application US/09436063C
Sequence 5. Application US/09436063C
SEDICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TILLE OF INVENTION: Methods Related Thereto
TITLE OF INVENTION: Methods Related Thereto
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILLING DATE: 1999-11-08
FRIOR PILLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1917
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                 Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.1%; Score 53.5; DB 4; Length 1917; Best Local Similarity 60.0%; Pred. No. 1e+02; Matches 9; Conservative 0; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.7%; Score 53; DB 4; Length 1652; Best Local Similarity 47.1%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 9; Indels
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: October 26, 2004, 15:41:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09627650B ; Patent No. 6406872
                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; Caenorhabditis elegans US-09-436-063C-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 crcrcr-crcrcrcr 80
                                                 3 CRCICTRGFCRCICT 17
                                                                              67 crcrcr-crcrcrcr 80
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US-09-627-650B-1
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2004, 15:15:31 ; Search time 23.5 Seconds (without alignments) 73.698 Million cell updates/sec Run on:

116 1 GFCRCICTRGFCRCICTR 18 US-10-009-317A-32 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	h DB ID Description	2	2 AS9089 theta defension	2 E71602 nrobable integra	2 G72858	2 T24272 hypothe	2 T15651 hypothe	2 JC1066	1 TIMB trypsin	2 S69207 vascular	2 S07405 proteinas	2 JC2225 Bowman-Birk	1 TISYC2 proteinase i	1 S54581 probable me	2 T18975	2 A25964 thyroglobulin - r	2 S08167 Balbiani	1 TIZB1P ·	1 TIZBIA proteinas	1 TIFB2 proteinase	2 S07941 proteinase	1 TISYD2 proteinase	2 T25185	2 S32834	2 JC5042	1 JH0675	2 I48725	2 PQ0618 . hypothetical pr	0,000
	Length			2	N		186	73	7.	418	80	8	103	624	152	157	1700	72	78	7	83	102	160	306	476	1353	77	550	
æ	Query Match	75.0	55.2	47.0	46.6	45.7	45.7	ů.	44.0	4.	43.5	43.5	43.5	43.1	42.2	42.2	42.2	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4		40.9	c
	Score	٦,		54.5	4		53	52.5	51		50.5	0	0	20	49	49	4	48	48	48	48	48	48	48	48		47.5		47
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tenomodulin - mous hypothetical prote hypothetical prote hypothetical prote gp30 protein prec	related to mutanas related to mutanas reelin precursor - proteinase inhibit - hypothetical prote	44 0	gene serrate prote EF1 protein - fowl
JC7603 T34264 T15840 T22945 T42737	149781 S58870 S09415 T17298	T09052 C96719 A57293 G96711	S16148 A31685
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317 29946 3191 4660	883 3461 146 511	761 792 1251 1307	1408
4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0	40.4 40.08 7.08.	300.7 200.7 200.7	39.7
44444. 777777	2.94 2.5 2.5 4.0	4 4 4 4 6 6 6 6	45.5
6 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	3337	4 4 4 4 0 1 2 6	4.4 5.

ALIGNMENTS

RESULT 1 (C59089 theta defensin-1 - rhesus macaque N;Alternate names: RTD-1 C;Species: Macaca mulatta (rhesus macaque) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: C59089	R;Tang, Y.Q; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.; Science 286, 498-502, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Reference number: A59089; MUID:99453140; PMID:10521339 A;Accession: C59089 A;Statuus: preliminary A;Molecule type: protein A;Residues: 1-18 <sel></sel>	A,Note: this sequence is cyclically permuted by -6 residues from the sequence presented : C,Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089. C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing F;1-9/Region: theta defensin la-derived F;10-18/Region: theta defensin la-derived F;10-18/Region: theta defensin la-derived F;1-18/Cross-link: cyclopeptide (Arg-Cyt) #status experimental F;2-11,4-9,13-18/Disulfide bonds: #status experimental F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental	Query Match 75.0%; Score 87; DB 2; Length 18; Best Local Similarity 86.7%; Pred. No. 0.00014; Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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4 RCICTRGFCRCICTR 18 දු දු

Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative

ð g RESULT 3

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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
St.Sims, M.
St.Sims, M.
Submitted to the EMBL Data Library, October 1995
A;Accession: T24272
A;Accession: T24272
A;Accession: T24272
A;Accession: T24272
A;Accession: T24272
A;Botous: preliminary; translated from GB/EMBL/DDBJ
A;Botous: Lof4 <MIL>
A;Residues: 1-164 <MIL>
A;Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T03
A;Accession: C:Genetics:
A;Gene: CESP:T01B7.8
A;Map position: 2
A;Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C27A2.5 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Accession: T15651
R,Nhan, M.
Sibmitted to the EMBL Data Library, May 1996
A,Recreption: The sequence of C. elegans cosmid C27A2.
A,Accession: T15651
A,Accession: T188 ANHA>
A,Accession: T188 ANH
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Cyspecies: Vigna radiata (mung bean)

Cyspecies: Vigna radiata (mung bean)

Cyspecies: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000

Cypace: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000

Cypace: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000

Cypace: 0.2 Nao, 0.F.; Zhang, M.F.; Dai, 0.F.

Chinese 0. Distochhol: 95 54-60, 1993

Ayritle: Synthesis of mung bean trypsin inhibitor by the combination of the single strand Ayrecsion: 001066

Ayroccesion: 001066
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C)Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C)Superfamily: Bowman-Birk proteinase inhibitor
C)Keywords: serine proteinase inhibitor
F)2-73/Product: trypsin inhibitor #status predicted «MAT»
F)14-40/Domain: Bowman-Birk inhibitor repeat homology «BBI»
F)14-66/Domain: Bowman-Birk inhibitor repeat homology
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Best Local Similarity 50.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%; Score 53; DB 2; 50.0%; Pred. No. 6.9;
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Best Local Similarity 50.03
Matches 9; Conservative
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A;Map position: 2
A;Introns: 19/3; 91/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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A;Residues: 1-248 <GAR>
A;Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AAC7197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residuss: 1.290 <AYR>
A;Cresiduss: 1.290 <AYR>
C;Genetics: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g559139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acorf-70 protein - Autographa californica nuclear polyhedrosis virus
C,Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A,Note: aboNA virus
C,Date: 12-Nov-1999
#sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C,Accession: G72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Viroloyy 202, 586-605, 1994
A,Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus, A,Accession: G72858
A,Accession: G72858
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cydcession: E71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
R;Gardner, M.J.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID: 99021743; PMID: 9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                             F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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46.6%; Score 54; DB 2; Length 290;
Best Local Similarity 40.7%; Pred. No. 7.7;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                            Score 64; DB 2; Length 76;
Pred. No. 0.2;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 FARCFCINTMOCFCPROGYKCECICRR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FCRCICT-----RGF-CRCICTR 18
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163 CSCICT---CTCICS 174

A, Gene: Acorf-70

RESULT 5

3 CRCICTRGFCRCICT 17

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A; Experimental source: clone 3D7

A;Gene: PFB0950w

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A;Residues: 'X',104-120 <JOU2>
Klee, J', Gray, A.; Yuan, J'; Luch, S.M.; Avraham, H.; Wood, W.I.
Submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and spe
A;Reference number: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g16996, A,Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translatist; B,Page (JM.), Kim, S.I. submitted to the EMBL Data Library, October 1992.
A;Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase inhibitor (Bowman-Birk) C-II - soybean C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Species: O2-lec-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29608; $29608; $40113
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-83 <GTO>
A;Residues: 1-83 <GTO>
A;Cross-references: EMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology C;Keywords: serine proteinase inhibitor
F;22-48/Domain: Bowman-Birk inhibitor repeat homology <BBl>
F;49-74/Domain: Bowman-Birk inhibitor repeat homology <BBl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AjGene: GDB:VEGFC; VRP
AjCross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;1-3.102/Domain: propeptide #status predicted <PRO>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568
R;diordano, A.; DellaGonne, M.; Pogher, C.; Marchetti, S.
submitted to the EMBL Data Library, December 1993
A;Description: Nuclectide sequence encoding a soybean C-II proteinase inhibitor.
                                                                                                                                                                               A,Accession: S69208
A,Molecule type: mRNA
A,Residues: 1-419 -LEBA
A,Cross-references: BMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R,Morrits, J.C.
A,Reference number: H01557
A,Recession: G02659
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-419 -MORA
A,Residues: 1-419 -MORA
A,Cross-reference: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.0%; Score 51; DB 36.0%; Pred. No. 22; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 CQCVCKRTCPRNQPLNPGKCACECT 363
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A;Accession: S07405
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-83 <JOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S29559
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A; Accession: 840113
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A, Molecule type: mRNA
A, Residues: 1-83 <BAE>
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Matches
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N.Alternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Abecelson: 563207; 561795; 571443; 569208; 602559
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, EMBO J. 15, 1751, 1996
A;Fitle: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for A;Reference number: S69207; MUID:96203094; PMID:8612600
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A; Molecule type: mRNA
A; Molecule the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Molecule the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Molecule this is a revision to the sequence from reference S61795
EMBLO 3 15, 290-298, 1996
A; Molecule this is a revision to the sequence from reference S61795
EMBLO 4 15, 290-298, 1996
A; Mille: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Fit4 (VA)
A; Molecule number: S61795; MUID: 96178224; PMID: 8617204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d Lys-1, respectively
Cycomment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
Cycomment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
Cycomment: This inhibitor series inhibitor series inhibitor repeat homology cBB1>
F;13-39/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;40-65/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;20-56/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;20-65/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;20/Inhibitory site: Lys (trypsin) #status predicted
F;20/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: three isoinhibitors are also found whose amino ends differ slightly from that
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A;Note: this sequence has been revised in reference S69207 A;Note: this sequence has been revised in reference S69207
                                                                                  <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                          Livysin inhibitor (Bowman-Birk) - mung bean C; Species: Vigna radiata (mung bean)
C; Species: Vigna radiata (mung bean)
C; Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C; Accession: A01301
S; Zhang, Y; Luo, S; Tan, F; Qi, Z; Xu, L; Zhang, A.
Sci. Sin. 25, 268-277, 1982
A; Title: Complete amino acid sequence of mung bean trypsin inhibitor.
A; Reference number: A01301
                                                                                  Gaps
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                                                                              Indels
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Score 52.5; DB Pred. No. 4.6; 3; Mismatches
                                            4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%; Score 51; DB 1
57.9%; Pred. No. 6.8;
iive 2; Mismatches
                                                                                                                                      3 CR-CICTR---GFCRCI----CTR 18
                                                                                                                                                                                                                 65
                                                                                                                                                                               CKSCICTRSMPGKCRCLDT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 1-72 <ZHA>
A,Cross-references: UNIPROT:P01062
   45.3%;
Query Match
Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.9
1es 11; Conservative
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Matches
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A; Molecule type: protein

DB 2;

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A;Molecule type: DNA
A;Residues: 1-431 <HUN>
A;Residues: 1-431 <HUN>
A;Cross-references: UNIPROT: PS4074; EMBL: Z49702; NID: G817859; PID: G1326013; GSPDB: GN0001:
A;Experimental source: strain AB972
B;Lye, G.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54014
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Taesort-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18975
B;McMurray, A.
Submitted to the EMBL Data Library, June 1995
A;Reference number: Z19054
A;Recence number: Z19054
A;Recence number: T18975
A;Recence number: T18975
A;Recence number: J18975
A;
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A;Residues: 345-624 <LYE>
A;Crese references: EMBL:Z49273; NID:g809577; PID:g809578; GSFDB:GN00013; MIPS:YMR119w
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YMR119w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YM8564.01; hypothetical protein YM9718.18
C;Speciaes: Saccharomyces cerevisiae
C;Speciaes: Saccharomyces cerevisiae
C;Accession: S54581; S54488
F#Hurt, S; Bowman, S
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
                                   F,42-68/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;69-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;64-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted F;49/Inhibitory site: Ala (elastase) #status predicted F;76/Inhibitory site: Arg (trypsin) #status experimental
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                                                                                                                                                                                                                                                                                         Length 103;
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Best Local Similarity 42.3%; Pred. No. 39;
Matches 11; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Generi MIDS:YMR119w
A.Map position: 13R
C.Superfamily: probable membrane protein YMR119w
C.Superfamily: probable membrane protein
F.82-98/Domain: transmembrane #status predicted <TM1>
F.120-136/Domain: transmembrane #status predicted <TM2>
F.211-227/Domain: transmembrane #status predicted <TM3>
F.231-253/Domain: transmembrane #status predicted <TM3>
F.237-253/Domain: transmembrane #status predicted <TM3>
F.237-253/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                     43.5%; Score 50.5; D
58.8%; Pred. No. 10;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 CRCFAICEDCRISLGLRGFSTCVCCR 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CRC--IC-----TRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 RCACTRSMPGQCRCLDT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RCICTR---GFCRCICT 17
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S54488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: S54581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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C;Species: Glycine max (soybean)
C;Accession: 072228
R;Back, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Bisack, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
A;Title: Nucleotide sequence homology of coNRs encoding soybean Bowman-Birk type protein A;Reference number: JC2224; MUID:94289861; PMID:7764974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-94 <BAE>
C;Comment: This protein regulates endogeneous proteinase during germination, stores sulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A22636
A;Molecule type: DNA
A;Molecule type: DNA
A;Cosiones: 1-103 «HAM»
A;Cross-references: UNIPROT:P01063; GB:K01967; NID:g169942; PIDN:AAA33952.1; PID:g169943
R;Odani, S.; Ikenaka, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Odani, S.; Ikenaka, T.
J. Biochem. 82, 1523-1531, 1977
A;Ittle: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a sq
A;Reference number: A01302; MUID:78087480; PMID:599141
A;Reference number: A01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Molecule type: protein
A.Residues: 28-103 <0DA>
C.Coment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interal
C.Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C.Keywords: duplication; seed; serine proteinase inhibitor
F.1-27/Domain: signal sequence #status predicted <SIG>
F.227/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: duplication; seed; serine proteinase inhibitor
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-94/Product: Bowman-Birk proteinase isoinhibitor C-II #status predicted <MAT>
F;39-59/Domain: Bowman-Birk inhibitor repeat homology <BBI>
F;60-85/Domain: Bowman-Birk inhibitor repeat homology <BBI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                               Gaps
                                                                                                                               ..
m
                                   43.5%; Score 50.5; DB 2; Length 83; 58.8%; Pred. No. 9.6; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 43.5%; Score 50.5; DB 2; Length 94; Local Similarity 58.8%; Pred. No. 9.4; es 10; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinase inhibitor (Bowman-Birk) C-II precursor - soybean
                                                                                                                                                                                                                                                                                     51 RCACTRSMPGQCRCLDT 67
                                                                                                                                                                                                          4 RCICTR---GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RCACTRSMPGQCRCLDT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RCICTR---GFCRCICT 17
Query Match
Best Local Similarity 58.0.
The local Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: JC2225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Start codon: GTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    7
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A;Gene: CESP:C06A1.6 A;Map position: 2 A;Introns: 22/3

thyroglobulin - rat (fragments)

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proteinase inhibitor (Bowman-Birk) II - kidney bean (tentative sequence)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 30-Nov-1880 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01299
R;Wilson, K.A.; Laskowski Sr., M.
J. Biol. Chem. 250, 4261-4267, 1975
A;Fitle: The partial amino acid sequence of trypsin inhibitor II from garden bean, Phasec A;Reference number: A01299; MUID:75151596; PMID:1126951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Vigna angularis (adzuki bean)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A01300
S;Kiyohara, T.; Yokota, K.; Masaki, Y.; Matsui, O.; Iwasaki, T.; Yoshikawa, M.
S;Kiyohara, 90, 721-728, 1981
A;Title: The amino acid sequences of proteinase inhibitors I-A and I-A' from adzuki beans
A;Reference number: A01300; MUID:82075699; PMID:7309695
                        C;Species: Vigna angularis (adzuki bean)
C;Date: 31.Mar-1992 #text_change 09-Jul-2004
C;Date: 31.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: C01300; A01300
C;Accession: C01300; A01300
T; Masaki, T.; Masaki, T.; Masaki, T.; Yoshikawa, M.
J; Sicohem: 90, 721-728, 1981
A;Title: The amino acid sequences of proteinase inhibitors I-A and I-A' from adzuki beans
A;Reference number: A01300; MUID:82075699; PMID:7309695
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: C01300
A, Molecule type: protein
A, Residues: 1-72 KIX>
A, Cross-references: UNITROT: P01061
A, Cross-references: UNITROT: P01061
C, Comment: This inhibitor strongly inhibitor; Bowman-Birk proteinase inhibitor:
F, Superfamily: Bowman-Birk proteinase inhibitor:
F, 13-50 F, Domain: Bowman-Birk inhibitor repeat homology ABB>
F, 40-65/Domain: Bowman-Birk inhibitor repeat homology ABB>
F, 20-65/Domain: Bowman-Birk inhibitor stress predicted
F, 20/Inhibitory site: Lys (trypsin) #status predicted
F, 47/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Comment: This inhibitor strongly inhibits trypsin.
C.Comment: This inhibitor strongly inhibits trypsin.
C.Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology C.Keywords: duplication; serine proteinase inhibitor repeat pomology <BB1>
F.46-71/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F.16-72,19-34,22-68,432,42-49,46-61,51-59/Disulfide bonds: #status predicted
F.56/Inhibitory site: Lys (trypsin) #status experimental
F.53/Inhibitory site: Arg (trypsin) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
41.4%; Score 48; DB 1; Length 72;
Best Local Similarity 52.6%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 2; Indels
- adzuki bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteinase inhibitor (Bowman-Birk) I-A - adzuki bean C; Species: Viqna anqularis (adzuki bean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
      proteinase inhibitor (Bowman-Birk) I-A'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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A, Molecule type: protein
A, Residues: 1-78 <KIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Species: Sattus norvegicus (Norway rat)
C;Date: 20-Unn-1889 #sequence_revision 30-Jun-1891 #text_change 11-Apr-1997
C;Date: 20-Unn-1889 #sequence_revision 30-Jun-1891 #text_change 11-Apr-1997
C;Date: 20-Unn-1889 #sequence_revision 30-Jun-1891 #text_change 11-Apr-1997
C;Date: 20-Unn-1889 #sequence_revision 33-327, 1886
C;Date: 20-Unn-1880 # 323-327, 1886
A;Title: The complete structure of the rat thyroglobulin gene.
A;Reference number: A2964; MUID:86094383; PMID:3455768
A;Recession: A2564
A;Recession: A2964
A;Recess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babliani ring 3 protein - midge (Chironomus tentans)
C,Species: Chironomus tentans
C,Species: Chironomus tentans
C,Species: Chironomus tentans
C,Accession: S08167
C,MUD:90172404; PMID:1689777
C,Accession: S08167
C,Accession: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 42.2%; Score 49; DB 2; Length 157; Local Similarity 32.0%; Pred. No. 20; and 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                           Query Match
42.2%; Score 49; DB 2; Length 152;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Indels
Matches 8; Indels
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g

Query Match

Best Loc Matches

RESULT 17 TIZB1P

3 CRCICTRG---

---FCRCIC 16

42.2%;

Query Match
Best Local Similarity 23.3
Matches 7; Conservative

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A;Nolecule type: protein
B;Chem. 267, 1990-1994, 1992
A;Title: Reactive sites of an anticarcinogenic Bowman-Birk proteinase inhibitor are simil
A;Nolecule cnumber: A42052; MUID:92112932; PMID:1730730
A;Reference number: A42052; MUID:92112932; PMID:1730730
A;Reference number: A42052; MUID:92112932; PMID:1730730
A;Contents: annotation; X-ray crystallography of inhibitor PI-II at 2.5 angstroms
C;Comment: This protein regulates endogeneous proteinase during germination, stores sulf,
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology (SIG)
F;127/Domain: signal sequence #status predicted (SIG)
F;28-102/Product: proteinase inhibitor repeat homology (BB)
F;44-70/Domain: Bowman-Birk inhibitor repeat homology (BB)
F;43-97,44-59,47-93,49-57,6774,71-86,76-84/Disulfide bonds: #status experimental
F;51/Inhibitory site: Arg (trypsin) #status predicted
F;78/Inhibitory site: Arg (trypsin) #status predicted
                                    A Experimental source: clone pB26
R:Odani, S.; Ikenaka, T.
B:Odani, S.; Ikenaka, T.
B:Ochem. 83, 737-745, 1978
A;Title: Studies on soybean trypsin inhibitors. XII. Linear sequences of two soybean dout A;Reference number: A01303; MUID:78150870; PMID:641033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPRCT: Q9XU68; EMBL: Z83127; PIDN: CAB05630.1; GSPDB: GN00022; CESP: T2:
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methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae
C;Species: Methanococcus voltae
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: S32834; S16726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T23F6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Deceies: D-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25185
R;Lloyd, C.
Submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
A;Cross-references: EMBL:X68706; NID:g18571; PIDN:CAA48657.1; PID:g18572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 2;
Pred. No. 27;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 CKCCOPVCTNACTNGGGCSCGCTR 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |:||| | |||: |
71 CKSCMCTRSQPGQCRCLDT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CR-CICTR---GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone T23F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%;
52.6%;
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Best Local Similarity 41.7%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: protein
A, Residues: 28-102 <001>
A, Accession: B01303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 76/3; 124/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Genetics:
A,Gene: CESP:T23F6.1
                                                                                                                                                                                                                                                                                                                                                A; Accession: A01303
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                                    A;Cross-references: UNIPROT:P01060
A;Note: two forms of the inhibitor were isolated; the amino end of the longer form is blashote: two forms of the inhibitor were isolated; the amino end of the longer form were sequenced only for the shorter form
C;Comment: This protein inhibits elastese and trypsin simultaneously and independently.
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology c;Reywords: blocked amino end; duplication; serine proteinase inhibitor
F;18-44/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;17-71,18-33,21-67,23-31,41-48,45-60,58/Disulfide bonds: #status predicted
F;25/Inhibitory site: Ala (elastase) #status experimental
F;52/Inhibitory site: Arg (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andreadus: 1.102 c80N>
;Residues: 1.102 c80N>
;Cross-references: UNIPROT:Q43709; EMBL:X68707; NID:g288618; PIDN:CAA48658.1; PID:g2886
;Back, J.M.; Songy, J.C.; Chol, Y.D.; Kim, S.I.
iosci. Biotechnol. Biochem. 58, 843-846, 1994
;Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type protein;Reference number: JC2224; MUID:94289861; PMID:7764974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P01064; EMBL:M20733; NID:g169946; PIDN:AAA33954.1; PID:g1699
(Subperfenally: Bowman-Birk protedinase inhibitor; Bowman-Birk inhibitor repeat homology
F;25-51/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;52-77/Domain: Bowman-Birk inhibitor repeat homology <BB12>
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N;Contains: proteinase inhibitor (Bowman-Birk) E-I (PI-II)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Accession: 53243, 402224; A01303; 829559
K;Song, J.C.; Back, J.M.; Kim, S.I.
submitted to the EMBL Data Library, October 1992
A;Reference number: 532243
A;Reference number: 532243
A;Accession: 532343
A;Accession: 532343
A;Accession: 532343
A;Accession: 53243
A;Accession: 54404
A;Ac
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C;Species: Glycine max (soybean)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: 807941
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the soybean protease inhibitors PI IV is a sequence of cDNA encoding the sequence of cDNA encoding t
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Pred. No. 16;
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Best Local Similarity 52.6%; Pred. No. 16;
Matches 10; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |:||| | |||: |
45 CKSCMCTRSMPGKCRCLBT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CR-CICTR---GFCRCICT 17
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Matches 10; Conservative
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A;Molecule type: mRNA
A;Residues: 1-83 <JOU>
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Africant type: mRNA
A;Residues: 1-1353 &NOE>
A;Residues: 1-1353 &NOE>
A;Residues: 1-1353 &NOE>
A;Rolecule type: mRNA
A;Residues: 1-1353 &NOE>
A;Rolecule type: mRNA
A;Residues: 1-1353 &NOE>
A;Rolecule type: protein
A;Residues: 579-586;827-840 &NOE1>
C;Comment: This protein is a neural extracellular matrix protein implicated in neural cel
C;Superfamily: restrictin; Ref homology; fibrinogen beta/gamma homology; fibronectin type
C;Comment: This protein is a neural extracellular matrix protein implicated in neural cel
C;Superfamily: restrictin; Ref homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprote
C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprote
C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprote
C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprote
C;Keywords: calcium binding; cells
F;10-329/Domain: EGF homology <EG3>
F;20-229/Domain: EGF homology <EG4>
F;20-229/Domain: EGF homology <EG4>
F;20-259/Domain: fibronectin type III repeat homology <FN3>
F;20-584/Domain: fibronectin type III repeat homology <FN5>
F;20-584/Domain: fibronectin type III repeat homology <FN5>
F;20-585/Domain: fibronectin type III repeat homology <FN5>
F;20-544/Domain: fibronectin type III repeat homology <FN5>
F;20-1027/Domain: fibronectin type III repeat homology <FN5>
F;20-1027/Domain: fibronectin type III repeat homology <FN6>
FN60-1027/Domain: fibron
                 restrictin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0675; PS0385; S23254
R;Nocrenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
A;Nocrenberg, U.; Wille, H.; Wolff, A.M.; Frank, R.; Rathjen, F.G.
A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with EG!
A;Reference number: JH0675; MUID:92265298; PMID:1375037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1035-1115/Domain: fibronectin type III repeat homology <FN9>
F;1130-1238/Domain: fibrinogen beteingamma homology <FRG>
F;1272-1286/Eggion: calcium binding #status predicted
F;53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0300 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148725
R;Wagner, S.; Cullmarn, G.; Knippers, R.
R;Wagner, S.; Cullmarn, G.; Knippers, R.
A;Title: The Q300 gene: a novel transcription unit induced in simian virus 40-infected ar
A;Reference number: 148725; MUID:91237845; PMID:1851876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: 148725
A;Status: proliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Acsidues: 1-77 <RES>
A;Cross-references: UNIPROT:Q02722; EMBL:X52164; NID:g53860; FIDN:CAA36417.1; FID:g53861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.9%; Score 47.5; DB 2; Length 77;
46.7%; Pred. No. 19;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 CRCICSEGWAGSNCS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CRCICTRGFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CRCICTRGFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 CVCVCV---CVCVCT 41
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Best Local Similarity 46.71
Matches 7; Conservative
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Query Match
Best Local Similarity 46.7%
Matches 7; Conservative
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A;Residues: 1-306 < kLbs.
A;Residues: 1-306 < kLbs.
A;Residues: 1-306 < kLbs.
A;Cross-references: UNIPROT:Q00406; EMBL:X61203; NID:g296614; PIDN:CAA43505.1; PID:g2966
A;Cross-references: UNIPROT:Q00406; EMBL:X61203; NID:g296614; PIDN:CAA43505.1; PID:g2966
R;Halboth, S.; Klein, A.
Submitted to the EMBL Data Library, August 1991
A;Peference number: S16721
A;Accession: S16726
A;Accession: S16726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-99, 'TR', 102-107,'P',126,'LH',129-306 <HAL>
A,Residues: 1-99, 'TR',102-107,'P',126,'LH',129-306 <HAL>
A,Residues: 1-99, 'TR',102-107,'P',126,'LH',129-306 <HAL>
B,Moles: references: EMBL:X61203
A,Note: the sequence is revised in GenBank entry X61203, release 117, (PIDN:CAA43505.1)
R,Halboth, S.; Klein, A.
Mol. Gen. Genet. 233, 217-224, 1992
A,Title: Methancoccus voltae harbors four gene clusters potentially encoding two [NiFe]
A,Reference number: A59304; MUID:92293118; PMID:1603063
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R;Isoai, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100, 1996
A;Title: Molecular cloning of a new member of the putative G protein-coupled receptor ge A;Reference number: JC5042; MUID:97074655; PMID:8917082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor - barnacle
C,Species: Balanus amphitrite (barnacle)
C,Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 41.4%; Score 48; DB 2; Length 476; Best Local Similarity 26.5%; Pred. No. 55; Mismatches 9; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: methyl viologen-reducing hydrogenase gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Klein, A.
submitted to the EMBL Data Library, August 1991
A;Reference number: S32833
AAcceseion: S32834
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В

Accession: JC5042

RESULT 25

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Query Match

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GB:AF219993
transmembrane protein on cell surface with an antianç
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F;255-317/Region: conserved carboxyl-terminus, homologous to chondromodulin-I #status pre
F;265-306/Domain: antiangiogenic #status predicted <ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:F46C8.4
A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507,
629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Blophys. Res. Commun. 280, 1323-1327, 2001
A;Title: Molecular cloning of tenomodulin, a novel chondromodulin-I related gene.
A;Reference number: JC7603; MUID:21092761; PMID:11162673
A;Contents: Embryo, 17-days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 C;Accession: JC7603 R;Shukunami, C.; Oshima, Y.; Hiraki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F46CB.4 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 29-0cr-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                           Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 317;
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A;Cross-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                     A;Map position: Xq22
C;Keywords: transmembrane protein
F;31-50/Domain: transmembrane #status predicted <TVM>
F;265-317/Region: highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core 47; DB 2;
red. No. 55;
Mismatches 5
                                                                                                                                                         Score 47; DB 2;
Pred. No. 55;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T34264
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                         263 GYCCIYCRGNRYCRRVC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 GYCCIYCRRGNRYCRRVC 280
                                                                                                                                                                                                                                                        1 GECRCICTEG--FCECIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: 09EP64;
C; Comment: Tenomodulin is a type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPCRCICTRG--FCRCIC 16
                                                                                                                                        Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4†
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-317 <SHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T34264
                                                                                                                                                                                                                                                                                                                                                                                                                                    tenomodulin
A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Yamana, K.; Wada, H.; Takahashi, Y.; Sato, H.; Kasahara, Y.; Kiyoki, M.
Biochem. Biophys. Res. Commun. 280, 1101-1106, 2001
A;Title: Molecular cloning and characterization of ChMiL, a novel member molecule simila
A;Reference number: JC7597; MUID:21092728; PMID:11162640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;Cross-references: UNIPROT:09H2S6
;Comment: This protein is a novel type II transmembrane protein which is similar to chd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATI) cDNAs from alfalfa leaves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypsin inhibitor precursor (clone ATI21) - alfalfa
Nylternate names: serine proteinase inhibitor
Cispecies: Medicago sativa (alfalfa)
Cispecies: Sef48; S49118
RymGurl, B.: Mukherjee, S.; Kahn, M.; Ryan, C.A.
Plant Mol. Biol. 27, 995-101, 1995
A;Title: Characterization of two proteinase inhibitor (ATI) cDNAs from alfala; A;Reference number: S86647; MUID:95284355; PMID:7766888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Species: Homo sapiens (man)
.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 550;
                                   Apothetical protein 550 - lactic dehydrogenase virus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; Length 113;
Pred. No. 28;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Keywords: serine proteinase inhibitor
F;56-113/Product: trypsin inhibitor #status predicted <MAT>
F;60-85/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;86-111/Domain: Bowman-Birk inhibitor repeat homology <BB12>
                                                                                                                                                                                                                                                                A, Reference number: JQ1990; MUID:93224885; PMID:8385693
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7
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Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCICT -----RG--FC-RCICTR 18
                                                                                                                                                                                                                                                                                         A, Accession: PQ0618
A, Molecule type: mRNA
A, Residues: 1-550 CHEA
A, Exos-references: UNIPROT: 083017; GB: L06812
A, Experimental source: isolate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chondromodulin-I like protein, ChMIL - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 CKSCICTRSYPPOCRC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 41.4:
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-317 <YAM>
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Cispecies: Ratture norvegicus (Norway rat)
Cipecies: Ratture norvegicus (Norway rat)
Cipecies: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
Cipacession: T42737
Risaito, A.; Pieterromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the A;Reference number: A58173; MUID:95024033; PMID:7937880
A;Accession: T472737
A;Accession: T47277
A;Accession: L47274
A;Accession: L47274
A;Accession: L47274
A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accessi
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A; Residues: 1-4660 <SAI>
A; Cross-references: UNIPROT: P98158; EMBL: L34049; NID: 9561852; PID: 9561853; PIDN: AAA51369.
A; Cross-references: UNIPROT: P98158; EMBL: L34049; Kidney
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-4660/Product: 99330 protein #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C'Accession: T49781 F. Farmann, B.; Holland, R.; Nyakatura, A.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000 A;Reference number: Z25022
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-883
A;Crsidues: 1-883
A;Crsis-references: UNIPROT:09P563; EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.180
A;Experimental source: BAC clone B9J10; strain OR74A
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33883
R;Courtney, L.; Langston, L.; Maupin, R.
submitted to the RML Data Library, February 1999
A;Description: The sequence of C. elegans cosmid H23N18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related to mutanase (mutA) gene [imported] - Neurospora crassa
N;Alternate names: protein B9J10.180
C;Species: Neurospora crassa
C;Species: O2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.5%; Score 47; DB 2; Length 4660; Best Local Similarity 50.0%; Pred. No. 3.4e+02; Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-141 <COU>
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Matches 8; Conservative
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A; Map position: 5
A; Introns: 33/2; 80/1; 121/3
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rosidues: 1-3191 <WIL>
A;Cross-references: UNIPROT:001335; EMBL:281094; PIDN:CAB03155.1; GSPDB:GN00023; CESP:TC
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A.Introne: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3; 1d
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AjMoLecule type: DNA
Asesidues: 1-2946 <br/>CDZ>
AjCross-references: EMBL:U40410; NID:g1065453; PID:g1065455; PIDN:AAA81392.1; CESP:C54G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:C54G7.3
A;Introns: 16/1; 53/2; 92/1; 160/3; 295/1; 346/1; 392/1; 440/1; 475/3; 579/1; 615/3; 169
46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3
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A;Residus: 1-3191 <WIZ>
A;Cross references: EMBb:z81110; PIDN:CAB03261.1; GSPDB:GN00023; CESP:T01D3.1
A;Experimental source: clone T01D3
                                                                                                                                                                                                        hypothetical protein C54G7.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C.Accession: T15840
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C.Species: Caenorhabdditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22945; T24295
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                                                                                                                                                                                                                                                                                                                                                                                     R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C54G7.
A;Reference number: Z18416
A;Reference number: Z18416
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submitted to the EMBL Data Library, October 1996
A;Reference number: 219870
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A,Reference number: Z19640
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T42737
gp330 protein precursor - rat
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2430 VCTNGFCHC 2438
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1215 VCVNGFCRC 1223
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C;Accession: T09052
F;Aibuchi, T.; Luscombe, M.; Elder, P.A.; Knowles, M.A.
Genomics 48, 277-288, 1998
A;Title: Structure and methylation-based silencing of a gene (DBCCRI) within a candidate A;Reference number: 216537; MUID:98207242; PMID:9545632
A;Ceesion: T09052
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A,Cross-references: UNIPROT.060477; EMBL:AF027734; NID:g3041876; PIDN:AAC39691.1; PID:g3(
A,Experimental source: tissue type: brain; developmental stage: fetal and infant
                                                                                                                                                                            hypothetical protein DKFZp586M2123.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T17299
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18729
A;Reference number: Z18729
A;Reference perlainary
A;Rocession: T17298
A;Reference number: Z18729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein DBCCR1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9NS15; EMBL:AL117551
A;Experimental source: adult uterus; clone DKFZp586M2123
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Job time : 33.5 secs
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Best Local Similarity 53.8
Matches 7; Conservative
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A; Map position: 9q32-q33
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reelin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mos musculus (house mouse)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003
C;Accession: S58970; S71844; 149297
R;D'Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.
Alvatre 374, 719-723, 1995
A;Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
A;Reference number: 149297; MUID:95231649; PMID:7715726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dioteinase inhibitor - cowpea
C;Species: Vigna unguiculata (cowpea)
C;Species: Vigna unguiculata (cowpea)
C;Aacession: 809415
R;Hilder, V.A.; Barker, R.F.; Samour, R.A.; Gatehouse, A.M.R.; Gatehouse, J.A.; Boulter,
Plant Mol. Biol. 13, 701-710, 1989
A;Title: Protein and cDNA sequences of Bowman-Birk protease inhibitors from the cowpea (A;Reference number: 809414; MUID:91370854; PMID:2491685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-146 <HIL>
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Superfamily: Bowman-Birk inhibitor repeat homology <BB1>
F;85-111/Domain: Bowman-Birk inhibitor repeat homology <BB2>
                                                                                                                                                                                                                                                    ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S71844
A;Molecule type: mRNA
A;Residues: 1-215, '7.17-1905,'S',1907-3355,'V',3357-3391,'N',3393-3461 <DA2>
A;Residues: 1-215, '7.27-1905,'S',1907-3355,'V',3357-3391,'N',3393-3461 <DA2>
A;Cross-references: EMBL:U24703; NID:9902486; PID:9902487
F;1-27/Domain: signal sequence #status predicted <&IG>
F;28-3461/Product: reelin #status predicted <WAT>
F;1769-1795/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.1%; Score 46.5; DB 2; Length 3461; Best Local Similarity 47.4%; Pred. No. 3.2e+02; Matches 9; Conservative 1; Mismatches 6; Indels 3.
                                                                                                                                                                                   Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.9%; Pred. No. 43;
Matches 9; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence not shown
Molecule type: mRNA
Residues: 1-3461 <DAR>
Cross-references: EMBL:U24703; NID:g902486; PID:g902487
                                                                                                                                                                 40.1%; Score 46.5; DB 2;
45.0%; Pred. No. 1.3e+02;
11ve 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D'Arcangelo, G.
Lumitted to the EMBL Data Library, April 1995
Reference number: 871844
                                                                                                                                                                                                                                                                                                                                                                  556 GLĆSFSĆNFĠFĊPIHSĊTĊT 575
                                                                                                                                                                                                                                                                                                 1 GFCRCICTRGFC---RCICT 17
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
C,Genetics:
A,Gene: NCSP:B9J10.180
A,Map position: 6
A,Introns: 26/3; 198/1
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ઠે g Gaps

; 0

Length 761;

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; 0

Indels

4

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model October 26, 2004, 15:13:05 Run on:

; Search time 115 Seconds (without alignments) 56.149 Million cell updates/sec

US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

2002273 segs, 358729299 residues

Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uol	Theta def	-~1		Rhesus th		Theta def	Anti-vira	Масаса ши	Cyclic de	Antimicro	Rhesus	Rhesus	Rhesus th				Rhesus th	12Y retro	IllY retr	Human ret	Human ret	Rhesus ma	Synthetic	Human ret	Enantio-r
	Description	Aab35046	Abp53295	Ado35230	Ado35240	Abp53299	Aab35030	Abp53297	Aae33866	Add95202	Add35357	Adg70012	Ado35229	Ado35238	Ado35239	Ado35250	Ado35263	Ado35255	Aae33805	Aae33806	Adn08180	Adn08181	Aab35037	Abp53294	Aae33801	Aae33863
0																										
SUPPERATES	ΙΩ	AAB35046	ABP53295	AD035230	AD035240	ABP53299	AAB35030	ABP53297	AAE33866	ADD95202	ADD35357	ADG70012	AD035229	AD035238	AD035239	AD035250	AD035263	AD035255	AAE33805	AAE33806	ADN08180	ADN08181	AAB35037	ABP53294	AAE33801	AAE33863
	DB	4	IJ	œ	ω	'n	4	ß	9	7	ω	ω	œ	œ	ω	œ	œ	œ	9	ø	ω	œ	4	Ŋ	9	9
	Length	18	18	18	18	18	18	, 18	18	18					18			18	18	18	18	18	18	18	18	18
ď	노르	100.0	100.0	100.0	95.7	88.8	-	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	7	87.1	86.2	80.2	80.2	80.2	80.2	78.4	77.6	77.6	77.6
	Score	116	116	116	111	103	101	101	101	101	101	101	101	101	101	101	101	100	693	6	93	93	91	90	06	90
	Result No.		8	m	゙゙゙゙゙゙゙゙゙゙゙゙゙゙	Ŋ	φ	7	æ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adn08176 Human ret	Ado35249 Rhesus th	Abp53298 Anti-vira	Aau91017 Transplan	Aae33864 Enantio-R	Aae33802 R9K retro	Adno8177 Human ret		-		N		Aae33804 I15Y retr	Aae33803 I6Y retro	Ado35256 Rhesus th	Adn08179 Human ret	Adno8178 Human ret	Aae33807 R4Y retro	Ado35246 Rhesus th	Ado35245 Rhesus th
8 ADN08176	8 ADO35249			6 AAE33864		8 ADN08177	4 AAB35047	5 ABP53296	8 ADO35231	8 AD035242	8 ADO35241	6 AAE33804	6 AAE33803		8 ADN08179	8 ADN08178	6 AAE33807	8 ADO35246	8 ADO35245
77.6 18	76.7 18	6.		1	0	7	7	1	1 1	-	74.1 18	3	.3		.3		.6	-	.6
26 90	27 89	6000	29 87				33 86	4	000	9 9	37 86	00		. 0	1 8		000	- α	ın.

ALIGNMENTS

The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue. Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses. Ouellette AJ; Ā Claim 15; Fig 16; 110pp; English. AAB35046 standard; peptide; 18 Yuan J, 99US-00309487. 10-MAY-2000; 2000WO-US012842. Theta defensin SEQ ID NO: 30. 27-MAR-2001 (first entry) (REGC) UNIV CALIFORNIA. Selsted ME, Tang Y, WPI; 2001-031853/04. WO200068265-A1. 10-MAY-1999; Unidentified 16-NOV-2000. AAB35046; RESULT 1 AAB35046

ŏ Sequence 18 AA;

Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels

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1 GFCRCICTRGFCRCICTR 18

ò g N

Anti-viral, viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor. New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus. Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28. Disclosure; Page 10; 65pp; English. ABP53295 standard; peptide; 18 AA 29-JAN-2002; 2002WO-US002435. 30-JAN-2001; 2001US-0265270P. 01-AUG-2001; 2001US-0309368P. (IOWA) UNIV IOWA RES FOUND. (first entry) Maury W, Stapleton J, WPI; 2002-674815/72. WO200260468-A2. Macaca mulatta 13-NOV-2002 38-AUG-2002 Synthetic. ABP53295 RESULT

The present invention describes a method (M1) of using a first anti-viral comprising a theta-defensin peptide in an amphipathic alphabatic peptide (I) comprising a theta-defensin peptide in an amphipathic alphabatic period a structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for inhibiting the growth and consideration of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS. reducing virus band diving percentage of VS in a contaminated tissue or fluid sample safe for use, or reducing the number of population regardless of virus infection status, or inducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, waine, cars, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who can infected with the virus, where the first anti-viral peptide is most preferably administered to a patient who is immunosuppressed to a subject who is cannotically, latently or acutely infected with the virus. The present sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention

Sequence 18 AA;

ö Gaps .; 0 Length 18; Indels Query Match 100.0%; Score 116; DB 5; Best Local Similarity 100.0%; Pred. No. 8.1e-06; Matches 18; Conservative 0; Mismatches 0;

GFCRCICTRGFCRCICTR 18

RESULT 3 AD035230

Ź ADO35230 standard; peptide; 18

AD035230;

(first entry) 15-JUL-2004

Rhesus theta defensin peptide, RTD-2.

Monkey, Rhesus theta defensin, RTD-2, antimicrobial peptide, cyclic, antimicrobial, antinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant, food preservative, bacterial infection, viral infection, disinfectant, fungal infection; haemolytic activity.

Macaca mulatta.

 1. 18 hotte= "The peptide is cyclised by a covalent link between these two residues" Location/Qualifiers Key Modified-site

Disulfide-bond Disulfide-bond Disulfide-bond

US2004014669-A1

Tack B;

Roller R, Mccray PB,

Stinski M,

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Example 1; SEQ ID NO 2; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03523-AD03527. The theta of detailed in the claims or appearing as AD03523-AD03527. The theta of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are also useful for treating surfaces, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the hardmicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2.

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Score 116; DB 8; Pred. No. 8.1e-06; 100.0%; Query Match Best Local Similarity

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Gaps .. 0

Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial; virucide, fungicide; food, contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; Indels ; 0 Rhesus theta defensin analogue peptide aRTD-2-OH. Mismatches /note= "Hydroxylated" Claim 1; SEQ ID NO 14; 46pp; English Location/Qualifiers ADO35240 standard; peptide; 18 AA ö 18 1 GFCRCICTRGFCRCICTR 18 30-APR-2002; 2002US-0377071P. 30-APR-2003; 2003US-00427715 1 GFCRCICTRGFCRCICTR (first entry) 18; Conservative (REGC) UNIV CALIFORNIA 3. .16 5. .14 7. .12 WPI; 2004-167945/16. Disulfide-bond Disulfide-bond Disulfide-bond Modified-site US2004014669-A1 Macaca mulatta 15-JUL-2004 Selsted ME, 22-JAN-2004 Synthetic AD035240; object. Matches RESULT 4 AD035240 셤

ö Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

Disclosure; Page 10; 65pp; English

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or sowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful to treating a patient suffering from the peptides are also activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.

Sequence 18 AA

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                                                                                                                                                                          Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
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                  Gaps
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                                                                                                                                                         Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32
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                                                                                                                                                                                                                                                                                                                                                        Stapleton J, Stinski M, Roller R, Mccray PB,
Length 18
                  1; Indels
Score 111; DB 8;
Pred. No. 2.7e-05;
                  Mismatches
                                                                                                     ABP53299 standard; peptide; 18 AA.
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                                     18
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                                                                                                                                                                                                                                                                                          29-JAN-2002; 2002WO-US002435
                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                         (IOWA ) UNIV IOWA RES FOUND
                                      1 GFCRCICTRGFCRCICTR
                                                 GPCRCTCTRGFCRCICTR
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-674815/72.
                                                                                                                                                                                                                            Macaca mulatta.
Synthetic.
                                                                                                                                                                                                                                                      WO200260468-A2
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                         13-NOV-2002
                                                                                                                                                                                                                                                                         08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                          Maury W,
                                                                                                                       ABP53299;
                                                                                    RESULT 5
ABP53299
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucles and anti-HIV activities, and can be used for inhibiting the growth and conce virus growth, infectivity burden, shed, and development of anti-configuration of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus is spread within a virally-infected subject (V8), reducing virus shed from a V3, reducing percentage of VS in a v8, reducing virus shed from a V3, reducing secretical alterory in a v8, reducing virus shed from a V3, reducing virus and infection status, or inducing latency in a v8, (b) reducing the infectivity of a virus; and (c) rendering virus.

CC population regardless of viral infection status, or inducing latency in a v8; (b) reducing the infectivity of a virus; and (c) rendering virus enterties of infections virus particles in a population of viruses. Wanne, contaminated tissue or fluid sample safe for use, or reducing the infectivity of a virus in sheep, cattle, horses, swine, costs, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is contaministered prior to or subsequent to the virus contacting the subject who is contaministered prior to or subsequent to the virus contacting the subject who is contaminated peptide is most preferably administered to a subject who is contaminated by latently or acutely infected with the virus acutely infected with the virus acutely infected with the virus anti-viral peptide is encourably administered to a subject who is contaminated by a contaminate of the virus contacting the percent of sequence represents a chimeric human invess,

us-10-009-317a-32.rag

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Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                             Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
                                                                                                                                                                                                                                                                         Stinski M,
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 10; 65pp; English
 ABP53297 standard; peptide; 18 AA
                                                                                                                                                                                                                       2001US-0265270P.
2001US-0309368P.
                                                                                                                                                                                                 29-JAN-2002; 2002WO-US002435
                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA RES FOUND.
                                         (first entry)
                                                                                                                                                                                                                                                                         Maury W, Stapleton J,
                                                                                                                                                                                                                                                                                              WPI; 2002-674815/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                           Macaca mulatta.
                                                                                                                                                        WO200260468-A2
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01-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                        Gaps
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                                                                                                                                                                                                                                                     Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
viral peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel theta defensin peptide with antimicrobial activity against
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                                                                                                                                                                                                                                                                                                                            "peptide bond cyclises the molecule"
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                                                    Length 18;
                                         Score 103; DB 5; Length 18 Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouellette AJ;
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                   AAB35030 standard; peptide; 18 AA.
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                                                   88.8%;
88.9%;
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                                                                                                               1 GICRCICTRGFCRCICGR
                                                                                            1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                 Theta defensin SEQ ID NO: 1,
                                                                                                                                                                                                           (first entry)
                                              Cuery Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                   1. .18
/note= 3
3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
Disulfide-bond
Disulfide-bond
                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                               WO200068265-A1
                                                                                                                                                                                                           27-MAR-2001
                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1999;
                                                                                                                                                                                                                                                                                                                 Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-2000.
           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                             RESULT 6
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ä

Mccray PB,

Roller R,

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphababilitical structure in a lighd environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-HIV activities, and can be used to rival resistance. (I) can be used for inhibiting the growth and so can be used for inhibiting the growth and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus is shed from a VS, reducing percentage of VS in a virus shed from a VS, reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus particles in a population of viruses. (M1) is useful for tractions virus particles in a population of viruses. (M1) is useful care reducing the infectivity of a virus in sheep, cartle, horses, swine, cats, fowl and humans e.g. an enveloped virus infection humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a partient who is immunosuppressed to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is acquence represents a rheam monthly infected with the virus, preferably administered to a subject who is subject who is contacting the virus peptide is acquence represented a resume monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention of the present inven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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Pred, No. 0.0003;
1, Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFCRCLCRRGVCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GECRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
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GFCRCLCRRGVCRCICTR 18

g

RESULT 7 ABP53297

Location/Qualifiers

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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD35357
HXXXH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modalling and screening novel antiblotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RIDI peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial infection, human pathogen, holin, defensin,
peptide nucleic acid, PNA, penicillin, tetracycline, ampicillin,
kanamycin, antibiotic, antibacterial, antibiotic-resistance gene, cyclic.
                                                                                                         Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                      New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

87.1%; Score 101; DB 6; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                              Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                     AAE33866 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                               Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                          transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVCRCICTRGFCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD95202 standard; peptide; 18
                                                                                                                                                                                                                              18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                                   18-APR-2001; 2001US-0284855P
                                                                                     Macaca mulatta RTD1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclic defensin fragment.
                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                             Lehrer RI, Waring AJ,
                                                                                                                                                                                                                                                                                                                   WPI; 2003-103387/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                               Macaca mulatta.
                                                                                                                                                                                     WO200285401-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                               16-APR-2003
                                           AAE33866;
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           AAE33866
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This invention describes a novel conjugate for treating prokaryotic infections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote cand intended for introduction into it. The prokaryote is a bacterium, capecially one pathogenic in humans. The transport mediator is preferably a human peptide or protein, especially a phage-holin protein, its acrive cargament or variant or a defension. The introduced compound is a peptide nucleic acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, tetracycline, ampicillin or kanamycin. The conjugate has the structure transport mediator-spacer-PNA where the spacer is poly(glycine and/or lysine), preferably containing 2-6 amino acids and the spacer is linked to the transport mediator through a cleavable disulfide bridge. The conjugates are administered together with an antibiotic, by parenteral, transdermal or subcutaneous routes. The products of the invention have antibacterial activity and are used, especially in combination with antibiotics, for treating prokaryotic, specifically bacterial, infections, especially where the pathogen is catabitate or easistance gene. Where the PNA is directed against the antibiotic resistance gene. Where the PNA is directed against consistant to co-administered antibiotics and then the bya is directed against constitute to co-administered antibiotics. 'e. 'old' antibiotics can be used successfully in cases where normally they would be ineffective. This sequence represents a cyclic defensin fragment described in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
                           1. .18
/note= "Residue 1 and residue 18 bond to form a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Braun K, Braun I, Debus J, Pipkorn R, Waldeck W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD35357 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 10; 34pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2003; 2003WO-DE000124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2002; 2002DE-01001862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFCRCICTRGFCRCICTR
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3..16
5..14
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                                                                                                                                   Disulfide-bond
Disulfide-bond
Disulfide-bond
Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                           WO2003059392-A2
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24-DEC-2003

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prostaglandin of the P-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intracoular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work symergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysphasia, irritial melancyte hyperplasia, and hyperplasmation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS; lipteitohnic acid; LTB, septic shock; antibacterial; fungicide; virucide; immunomodulator; anticoagulant activity; minomodulator; anticoagulant activity; microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
                                            antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridai malanocyte hyperplasia; hyperplamentation.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ophthalmic solution useful for the treatment of increased intraocular. pressure comprises a prostaglandin of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel ophthalmic solution comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 8; Length 18;
Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhesus theta-defensin-1 (RTD-1) peptide.
            Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG70012 standard; peptide; 18
                                                                                                                                                                                                                                         21-MAR-2003; 2003WO-US008935
                                                                                                                                                                                                                                                                           21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFCRCICTRGFCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 83.33
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                              (CAYM-) CAYMAN CHEM CO
                                                                                                                                                                                                                                                                                                                                                 Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-011506/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta
                                                                                                                                     Unidentified
                                                                                                                                                                                                        02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                   Maxey KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG70012;
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ADG70012
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This invention describes the novel use of rhesus theta defensin-1 (RTD-1) bacteraening a composition for treatment and/or prevention of bacteraenia for binding bacterial products such as lipopolysaccharide (LPS) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe infections caused by Gram-positive or negative bacteria and yeasts, or by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding), increasing release of tregulatory factors) and anticoagulant action, so provides a better and simpler treatment.
                                                                                                                                                                                                   Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monkey, Rhesus theta defensin, RTD-1, antimicrobial peptide, cyclic, antimicrobial, antinflammatory, antibacterial, virucide, fungicide: food; contact lens solution, eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative, bacterial infection, viral infection; disinfectant; fungal infection; haemolytic activity.

    18 /note= "The peptide is cyclised by a covalent link
between these two residues"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 8; Length 18;
Pred. No. 0.0003;
                                                                                                                                    Gerdes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                    Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                    Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                 30-MAY-2003; 2003WO-EP005694.
                                                                  13-JUN-2002; 2002DE-01026216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                   (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                    Ladel C, Newton B,
                                                                                                                                                                       WPI; 2004-071500/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2004
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Gaps

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Gaps

30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P.

US2004014669-A1

22-JAN-2004

(REGC) UNIV CALIFORNIA

Tran DQ;

Selsted ME,

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of survival of microorganism as well as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monkey, Rhesus theta defensin, RTD, antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection;
                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101, DB 8; Length 18;
Pred. No. 0.0003;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 1; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Hydroxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO35238 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%;
                                 30-APR-2003; 2003US-00427715.
                                                                 30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFCRCLCRRGVCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                        Tran DQ;
                                                                                                                                                                         WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rood preservative;
fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                        Selsted ME,
22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD035238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD035238
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or cod product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbisidal inhibition of survival of microorganism as well as incrobistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have betterial, viral, fungal or other infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbicatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                               Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a Rhesus theta defensin analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%; Score 101; DB 8; Length 18; 83.3%; Pred. No. 0.0003; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus theta defensin analogue peptide aRTD-1-NH.
                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 12; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO35239 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                              WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD035239;
                                                                                                                                                                                                                                                                                                                                                   object.
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ADO35239
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Query Match
Best Local Similarity 83.3%
The 15; Conservative
                                        Selsted ME, Tran DQ;
                                              WPI; 2004-167945/16.
            US2004014669-A1
                                                                                                                          Sequence 18 AA;
Disulfide-bond
Modified-site
                                                                                                                                                                                                          Macaca mulatta.
Synthetic.
                 22-JAN-2004
                                                                                                                                                                     AD035250;
                                                                                                                                                          RESULT 15
ADO35250
S
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defension analogue is useful for reducing as ADO35239-ADO35257. The theta defension analogue is useful for reducing or inhibiting growth or survival of a microcorganism in an environment capable of sustaining the growth or survival of the microcorganism and is useful for reducing or inhibiting or inhibiting growth or survival of a microcorganism in an environment such as food or food product, a solution (e.g., contact lens solution), or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbisidal inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a theta defensin analogue defined by formulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

    18 /note= "The peptide is cyclised by a covalent link
between these two residues"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 101; DB 8; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.0003;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monkey RTD-1 (rhesus theta defensin 1) 2X protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 24; 46pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD035263 standard; protein; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                  30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFCRCTRGFCICICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selsted ME, Tran DQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                            US2004014669-A1
                                                                                                                              Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                                                                                                        Disulfide-bond
     Key
Modified-site
                                                                                                                                                                                                                                                                22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD035263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          object.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting or orbit of the microorganism in an environment such as food or survival of a microorganism in an environment such as food or coop product, a solution of a microorganism in an environment such as food or solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the teating a patient suffering from the peptides are also useful for the teating a patient suffering from the peptides are also useful for the theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 8; Length 18;
Pred. No. 0.0003;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhesus theta defensin analogue peptide RTD-1-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 13; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO35250 standard; peptide; 18 AA.
                                                       /note= "Amidated"
                                                                                                                                                                                                            30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.1%;
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                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
7. .12
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or

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Gaps

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Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide, antimicrobial, antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.

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Rhesus theta defensin analogue peptide RTD-4.
                                                                                                                                                                                                   Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                    US2004014669-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                Macaca mulatta.
                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                              22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                 Selsted ME,
                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE33805
ID AAE3
XX
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD03527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganisms as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from this antimicrobial activity and low haemolytic activity. The present section may be activity and low haemolytic activity. The present and the antimicrobial activity and low haemolytic activity. The present and activity and low haemolytic activity. The present and activity and low haemolytic activity. The present and activity and low haemolytic activity.
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                                                                                                                                                                                                                                                                                                                                                                  Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 8; Length 38;
Pred. No. 0.00052;
1; Mismatches 2; Indels
                                                Location/Qualifiers
1. .2
1. .2
1. .2
2. .19
7. .19
7. .19
7. .19
                                                                                                                20. .21
/note= "CNBr cleavage site"
21. .38
/note= "RTD-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD035255 standard, peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 17a; 46pp; English.
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                                                                                                                                                                                                                                                       30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                               30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GFCRCLCRRGVCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 defensin, RTD-1 peptide
                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                        Tran DQ;
                                                                                                                                                                                                                                                                                                                                WPI; 2004-167945/16.
N-PSDB; ADO35262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 AA;
                 Macaca mulatta
                                                                                                                 Cleavage-site
                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2004
                                                                                                                                                                                                                                                                                                          Selsted ME,
                                                                                                                                                                                                       22-JAN-2004
                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD035255;
                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO35255
ID ADO3
XX
AC ADO3
XX
DT 15-2
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or coop product, a solution (e.g., contact lens solution, or eye wash colution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
Monkey; Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antilnflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps

    .18
/note= "The peptide is cyclised by a covalent link
between these two residues"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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86.2%; Score 100; DB 8; Length 18
Best Local Similarity 93.8%; Pred. No. 0.00038;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFCRCICTRGFCRCIC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-167945/16.
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Retrocyclin, infection, sexually transmitted disease, gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.

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form

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/note= "Linked to amino acid at position 1 to form cyclic structure"

/note= "Linked to amino acid at position 18 cyclic structure" 3. .16 7. .12

Disulfide-bond 3. . Disulfide-bond 5. . Disulfide-bond 7. . Misc-difference 18

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WO200285401-A1

31-OCT-2002

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Location/Qualifiers

Key Misc-difference

Unidentified

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The invention relates to novel retrocyclin peptides. Peptides and methods sof the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                          /note= "Linked to amino acid at position 18 to form cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                       /note= "Linked to amino acid at position 1 cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 6; Length 18;
Pred. No. 0.0021;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong TB;
                                                                                                                                                                         Location/Qualifiers
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                                                          retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 24; 72pp; English.
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                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                               Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                  WO200285401-A1
                              16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehrer RI,
AAE33805
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                               New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 6; Leus-
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Pred. No. 0.002
1; Mismatches
                                                                                                                                                                                                                                                                                                                                     TB;
                                                                                                                                                                                                                                                                                                                                      Hong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RC-104
                                                                                                                                                                                                                                                                                                                                     Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                        transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 24; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                                18-APR-2002; 2002WO-US012353
                                                                                                                                                                                                                                                                                       18-APR-2001; 2001US-0284855P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFCRCICTRGFCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADN08180 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                     Waring AJ,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-103387/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                     Lehrer RI,
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ADN08180
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06-MAY-2003; 2003WO-US014106 06-MAY-2002; 2002US-00141645

WO2004033479-A2

22-APR-2004

UNIV CALIFORNIA

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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic condending a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefension or retrocyclin to the cell; a method for killing microbial coranisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin to the microbial organisms; a method for administering restrocyclin as a microbial organism by administering nestrocyclin as a infection, and a method for administering retrocyclin as a prophlactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine infection such as HIV-1. The retrocyclin peptide can be used as a vaccine as therapeutic and prophlactic agents for treating and preventing as therapeutic and prophlactic agents for treating and prophlactic and control and viral infections. This sequence represents a retrocyclin
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                                                                                                                                                                                                                                                                                                                                                         New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.2%; Score 93; DB 8; Length 18; 77.8%; Pred. No. 0.0021; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         Cole AM, Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 5; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human retrocyclin peptide, RC-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADNO8181 standard; peptide; 18 AA
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                                                                                                                    06-MAY-2003; 2003WO-US014106.
                                                                                                                                                     06-MAY-2002; 2002US-00141645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microbial; viral; human.
                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
(LEHR/) LEHRER R I.
                                                                                                                                                                                                                                                                                         Lehrer RI, Waring AJ,
                                                                                                                                                                                                     MARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                                                                                                                          WPI; 2004-340883/31.
                                                 WO2004033479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
Homo sapiens.
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Synthetic.
                                                                                   22-APR-2004
              Synthetic.
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Matches
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ADNO8181
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Therrior further provides a cycle plot pettocyclin peptide. The intention further provides a cycle plot pettocyclin, an election in a cell by administering an effective dose of a circular infection in a cell by administering an effective dose of a circular minidefension or retrocyclin to the cell, a method for killing microbial organisms by administering an effective dose of retrocyclin to the organisms by administering an effective dose of retrocyclin to the organisms by administering an effective dose of retrocyclin as a therapeutic agent to a patient with an established microbial or viral infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine infection are defined by the peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
                                                                                                                                                                                                                                                                                                                         New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated retrocyclin peptide. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus macaque theta defensin peptide SEQ ID NO: 8.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 6; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35037 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                     Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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Best Local Similarity 77.00.
Conservative
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide of the invention.
                                                                                                                                                                                                                                                     Lehrer RI, Waring AJ,
                                                                                                                                                       (LEHR) LEHRER R I.
(WARI/) WARING A J.
(COLE/) COLE A M.
(HONG/) HONG T B.
                                                                                                                                                                                                                                                                                        WPI; 2004-340883/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
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(LEHR/)
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Ouellette AJ; Yuan J, Tang Y, WPI; 2001-031853/04. Selsted ME,

Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses. Example 1, Fig 2, 110pp, English

Novel theta defensin

The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives

Sequence 18 AA;

Gaps . 0 Length 18; Query Match
78.4%; Score 91; DB 4; Length 18;
Best Local Similarity 81.2%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 2; Indels

GFCRCICTRGFCRCIC 16 GFCRCLCRRGVCRCIC 18

RESULT 2: ABP53294

ABP53294 standard; peptide; 18

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(first entry) 13-NOV-2002

Synthetic anti-viral human theta defensin peptide HTD-1 SEQ ID NO:27

Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.

Homo sapiens Synthetic.

WO200260468-A2

08-AUG-2002

29-JAN-2002; 2002WO-US002435.

30-JAN-2001; 2001US-0265270P 01-AUG-2001; 2001US-0309368P

(IOWA) UNIV IOWA RES FOUND.

New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus. WPI; 2002-674815/72.

Tack B;

Mccray PB,

Roller R,

Stinski M,

Stapleton J,

Maury W,

Disclosure, Page 9, 65pp, English.

The present invention describes a method (M1) of using a first anti-viral peptide (1) comprising a theta-defensin peptide in an amphipathic alpha-helical structure in a lipid environment for reducing the infectivity of a virus. (1) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti

containing subject from be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus burden in a VS, reducing virus series of virus infected subject (VS), reducing virus burden in a VS, reducing virus series of viral infection status, or inducing latency in a CO VS, (b) reducing the infectivity of a virus; and (c) rendering virus of VS, (b) reducing the infectivity of a virus; and (c) rendering virus of infections virus particles in a population of viruses. (M1) is useful CO VS, (b) and humans e.g. an enveloped virus infecting humans such as chann immunodeficiency virus (HIV). Preferably, the anti-viral peptide is containistered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is containistered by a latently or acutely infected with the virus. The present sequence represents a human thera defensin anti-viral peptide, which is given in the exemplification of the present invention \$

Sequence 18 AA;

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Gaps ; 0 Score 90; DB 5; Length 18; Pred. No. 0.0043; 4; Indels 0; Mismatches 77.6%; 14; Conservative Best Local Similarity Query Match Matches

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1 GFCRCICTRGFCRCICTR 18

à g

1 GICRCICGRGICRCICGR

RESULT 24 AAE33801

AAE33801 standard; peptide; 18 AA. (first entry) 16-APR-2003 AAE33801;

Human retrocyclin peptide.

Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection, antibiotic modelling, antimicrobial; human; cyclic.

Homo sapiens

Location/Qualifiers Key Misc-difference 1

to form a

/note= "Linked to amino acid at position 18
cyclic structure" Disulfide-bond Disulfide-bond Misc-difference Disulfide-bond

/note= "Linked to amino acid at position 1 to cyclic structure"

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WO200285401-A1

31-OCT-2002

18-APR-2002; 2002WO-US012353

18-APR-2001; 2001US-0284855P

(REGC) UNIV CALIFORNIA

Hong TB; Cole AM, Waring AJ, Lehrer RI,

WPI; 2003-103387/09.

transmitted diseases, vaginosis

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                                                                                              The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroiral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
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Pred. No. 0.0043;
0; Mismatches 4; Indels
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1. .18
/note= "D-form residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enantio-retrocyclin peptide analogue.
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                                                                       Claim 9; Page 24; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        AAE33863 standard; peptide; 18
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                    1 GFCRCICTRGFCRCICTR
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Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
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Misc-difference
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                                                                                                                                                                                                                                   Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to the cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering sectionyclin as a therapeutic agent to a patient with an established microbial or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
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                                                                                                                                                                                                                                                           4; Indels
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Post Local Similarity 77.8%; Pred. No. 0.0043;
Matches 14; Conservative 0; Mismatches 4
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                          Disclosure; Page 24; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        AA.
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LEHRER R I.
WARING A J.
COLE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microbial; viral; human.
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and viral infections.
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(LEHR/)
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(COLE/)
(HONG/)
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us-10-009-317a-32.rag

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infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
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            8888888888888
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Score 90; DB 8; Length 18;
Pred. No. 0.0043;
0; Mismatches 4; Indels
                            0; Mismatches
                                                     18
                                                     1 GFCRCICTRGFCRCICTR
                            14; Conservative
                Local Similarity
                           Matches
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Gaps

18 GICRCICGRGICRCICGR

ADO35249 standard; peptide; 18 AA. RESULT 27 AD035249

ADO35249;

Rhesus theta defensin analogue peptide RTD-1-25.

(first entry)

is-JUL-2004

Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antiinflammatory, antibacterial, virucide, fungicide, food, contact lens solution, eye wash solution, inflammatory response, microbicidal inhibition, microbistatic growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, disinfectant fungal infection, haemolytic activity, cyclic.

Macaca mulatta Synthetic

 18 /note= "The peptide is cyclised by a covalent link between these two residues" Location/Qualifiers Modified-site

Disulfide-bond Disulfide-bond Disulfide-bond

US2004014669-A1

22-JAN-2004.

10-APR-2003; 2003US-00427715

30-APR-2002; 2002US-0377071P. (REGC) UNIV CALIFORNIA.

Selsted ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Claim 1; SEQ ID NO 23; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival

ö The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing surface, or a mammal. The microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the rapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide. Anti-viral, viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor. omprising a Theta-structure in a lipid Gaps œ Tack Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31 Roller R, Mccray PB, New method of using a first anti-viral peptide comprising defensin peptide in an amphipathic Alpha-helical structure environment for reducing the infectivity of a virus. 76.7%; Score 89; DB 8; Length 18; 77.8%; Pred. No. 0.0054; ive 0; Mismatches 4; Indels Stinski M, Disclosure; Page 10; 65pp; English. Ä 18 138 ABP53298 standard; peptide; 18 29-JAN-2002; 2002WO-US002435. 30-JAN-2001; 2001US-0265270P. 01-AUG-2001; 2001US-0309368P. 1 GFCRCICTRGFCRCICTR GFCRCRRRGVCLCICTR (IOWA) UNIV IOWA RES FOUND. (first entry) Local Similarity 77.8 Maury W, Stapleton J, WPI; 2002-674815/72. Sequence 18 AA; Macaca mulatta. Synthetic. WO200260468-A2. Homo sapiens 13-NOV-2002 08-AUG-2002. ABP53298; Query Match RESULT 28
ABP53298
AC ABP53298
XX ABP53298
XX ABP53298
DT 13-NC
XX ANT:
XX ANT Matches 88888888888888888888888 셤 à

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spread within a virally-infected subject (VS), reducing viral burden in a VS, reducing virus shed from a VS, reducing percentage of VS in a VS, reducing virus shed from a VS, reducing percentage of VS in a CS population regardless of viral infection status, or inducing latency in a VS, (b) reducing the infectivity of a virus; and (c) rendering virus-contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is the chronically, latently or acutely infected with the virus. The present sequence represents a chimeric human/rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transplant, antimicrobial peptide, pore forming agent, cardioplegia, cell surface receptor binding compound, kidney transplant, cardioplegia, organ transplant, transplant rejection, defensin.
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Pred. No. 0.0069;
1; Mismatches 4; Indels
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17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the media of the present invention for either three or four days had serum

Claim 8; Page 28; 78pp; English

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creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplanted fhealthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial defensin peptide studied in the development of the transplant media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
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3. .16
5. .14
7. .12
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                                                                                                                                                                                                                                    Query Match 75.0%; Score 87; DB 5; Length 18; Best Local Similarity 86.7%; Pred. No. 0.0088; Matches 13; Conservative 1; Mismatches 1; Indels
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1. .18
/note= "D-form residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAE33864 standard; peptide; 18
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Disulfide-bond
Disulfide-bond
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE33864;
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                                                                                                                                                                                                                                                                                                                                                                                                   AAE33864
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The invention relates to novel retrocyclin peptides. Peptides and methods sof the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modalling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                           Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. .16
5. .14
7. .12
                                                                                                                                                         Gaps
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Linked to amino acid at position 1 to
                                                                                                                                 Score 87; DB 6; Length 18;
Pred. No. 0.0088;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                     R9K retrocyclin peptide analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclic structure"
                                                                                                                                                                                18
                                                                                                                                                                                                                                                               AAE33802 standard; peptide; 18
                                                                                                                                  75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2002; 2002WO-US012353,
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                                                                                                                                                                                                     1 Gickcicskaickcicsk
                                                                                                                                                                                1 GFCRCICTRGFCRCICTR
                                                                                                                           Query Match 72.2'
Best Local Similarity 72.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200285401-A1
                                                                                                                                                                                                                                                                                                               16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2002.
                                                                                                                                                                                                                                                                                        AAE33802;
                                                                                                                                                                                                                                          RESULT 31
                                                                                                                                                                                                                                                     AAE33802
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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The

New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases.

English,

Hong TB;

Cole AM,

Waring AJ,

Lehrer RI,

WPI; 2003-103387/09

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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular mindefensin or retrocyclin to the cell; a method for killing microbial corganisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and method for administering restrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and infection such as HIV-1. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                              retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
                                                                                                                                     Gaps
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0
                                                                                     Score 87; DB 6; Length 15; Pred. No. 0.0088;
                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hong TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; SEQ ID NO 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Human retrocyclin peptide, RC-101.
                                                                                                                                                                                                                                                                                     ADNO8177 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole AM,
                                                                                                                                                                    18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2002; 2002US-00141645
                                                                                                ch 75.0%;
1 Similarity 72.2%;
13; Conservative
                                                                                                                                                                    1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                           GICRCICGKGICRCICGR
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV CALIFORNIA.
LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-340883/31.
                                                                                                  Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004033479-A2
                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                    ADN08177;
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(LEHR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WARI/)
                                                                                                                                                                                                                                                   RESULT 3:
ADN08177
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us-10-009-317a-32.rag

Page 17

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The present invention describes a method (MI) of using a first anti-viral comprising a theta-defensin peptide in an amphipathic alphace peptide (I) comprising a theta-defensin peptide in an amphipathic alphace peptide is structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HV activities, and can be used for includent and can be used for inhibiting the growth and conce virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS, reducing virus shed from a VS, reducing virus latency in a VS, reducing virus infections tatus, or inducing latency in a VS, (b) reducing the infectivity of a virus; and (c) rendering virus.

CC population regardless of viral infection status, or inducing latency in a CS infectious virus particles in a population of viruses. (MI) is useful of infectious virus particles in a population of viruses. (MI) is useful of reducing the infectivity of a virus; insheep, cattle, horses, swine, case, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is containistered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a patient whose the first anti-viral peptide is containistered to a patient whose the first anti-viral peptide is containistered to a patient whose the first anti-viral peptide is containistered to a patient where the first anti-viral peptide is containistered to a patient whose the first anti-viral peptide is contained by a patient whose the first anti-viral peptide is contacting the virus. The present section in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Mccray PB,
                                                                                                                                                                                                                                                                                                                                                                      Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhesus theta defensin peptide, RTD-3.
                                                                                                                                                                                                                                                                                                                                                                      Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO35231 standard; peptide; 18
                                                                                                                                                                                                                                                              30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
                                                                                                                                                                                                                     29-JAN-2002; 2002WO-US002435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVCRCLCRRGVCRCLCRR
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nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674815/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 18 AA;
                                                                    Macaca mulatta.
Synthetic.
                                                                                                                                   WO200260468-A2
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                                                                                                                                                                              08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                      Maury W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-viral; viral infection; theta-defensin; lipid environment;
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                                                               Score 87; DB 8; Length 18;
Pred. No. 0.0088;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                           AAB35047 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Fig 16; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP53296 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                        Selsted ME, Tang Y, Yuan J,
                                                                 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2000; 2000WO-US012842.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Theta defensin SEQ ID NO: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-1999; 99US-00309487
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hes 12; Conservative
                                                                                                                 Conservative
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                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200068265-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                      AAB35047;
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Matches
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                                                                                                                                                                                                                                                                     RESULT 33
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(first entry)

15-JUL-2004

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Disulfide-bond
Disulfide-bond
           Modified-site
                    22-JAN-2004.
                                    object.
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Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbicidation; microbicidation; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                          Rhesus theta defensin analogue peptide aRTD-3-NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 16; 46pp; English
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2002; 2002US-0377071P.
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                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                             Macaca mulatta.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   object.
The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism and is useful for reducing or inhibiting rowth or survival of the microorganism and is useful for reducing or inhibiting crowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbictatic inhibition of survival of microorganism as well as the appended are also useful for treating a peptides are useful as the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for when the section in the present of the information of sequence represents the rhesus monkey wild-type theta defensin RTD-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                  Monkey, Rhesus theta defensin, RTD-3; antimicrobial peptide, cyclic, antimicrobial; antinflammatory; antibacterial; virucide, fungicide; food; contact lens solution; eye wash solution; inflammatory response, microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps

    18 /note= "The peptide is cyclised by a covalent link
between these two residues"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 3; 46pp; English.
                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2002; 2002US-0377071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.,
Best Local 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                     US2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
                                                                                                                                                                             Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object compact lens solution, or eye wash solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as incrobistatic inhibition of growth. Thus the peptides are useful as microbistatic also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86; DB 8;
Pred. No. 0.011;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO35241 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Marches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
ADO35241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
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ADO35242 standard; peptide; 18 AA.

RESULT 36 ADO35242

δ 셤 AD035242

AAE33804 standard; peptide; 18 AA.

RESULT 38

(first entry)

16-APR-2003

defensin analogue peptide aRTD-3-OH.

(first entry)

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash colution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbiscatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                    Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial, antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant; food preservative; bacterial inflection; viral inflection; disinfectant; fungal inflection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 15; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004014669-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                          Macaca mulatta.
                                                                                        Rhesus theta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2002;
                                                     15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selsted ME,
                                                                                                                                                                                                                                                                           Synthetic
                 ADO35241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  object
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Tran DQ;

/note= "Hydroxylated"

Location/Qualifiers

3. .16 5. .14 7. .12

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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                              Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                           /note= "Linked to amino acid at position 18 to form a cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                             amino acid at position 1 to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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Best Local Similarity 72.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 5: Tndele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hong TB;
                                                                                                                                                                Location/Qualifiers
1
                                                                                                                                                                                                                                                                                           /note= "Linked to cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE33803 standard; peptide; 18 AA
                                                        I15Y retrocyclin peptide analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehrer RI, Waring AJ, Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmitted diseases, vaginosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 24; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2001; 2001US-0284855P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFCRCICTRGFCRCICTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                 3. .16
5. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-103387/09
                                                                                                                                                                                                                                  Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                           WO200285401-A1
                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE33803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
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Gaps . 0

Score 86; DB 8; Length 18; Pred. No. 0.011; 2; Mismatches 4; Indels

Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative

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16-APR-2003 (first entry)

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Rhesus theta defensin analogue peptide RTD-5.
                16Y retrocyclin peptide analogue.
                                                                                                                                                                                                                                                   Claim 9; Page 24; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                AD035256 standard; peptide; 18
                                                                                                                                                          18-APR-2002; 2002WO-US012353
                                                                                                                                                                     18-APR-2001; 2001US-0284855P
                                                                                                                                                                                                                                                                                                                                                        1 GFCRCICTRGFCRCICTR
                                                                                                                                                                                                                                                                                                                                                                   GICRCYCGRGICRCICGR
                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                             Lehrer RI, . Waring AJ,
                                                                                                                                                                                                        WPI; 2003-103387/09
                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                Key
Misc-difference
                                                                                             Disulfide-bond
Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                        Disulfide-bond
                                                                                                                                  WO200285401-A1
                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                             AD035256;
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
XEXHXXXX.
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash colution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbobicidal inhibition of growth. Thus the peptides are useful as the rapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the action of the persent defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
Monkey, Rhesus theta defensin, RTD; antimicrobial peptide, antimicrobial, antinflammatory; antibacterial, virucide, fungicide, food; contact lens solution, eye wash solution, inflammatory response; microbicidal inhibition, microbistatic growth inhibition; disinfectant, food preservative, bacterial infection; viral infection; disinfectant, fungal infection; haemolytic activity; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate

    .18

note= "The peptide is cyclised by a covalent link

between these two residues"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 85; DB E Pred. No. 0.014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 30; 46pp; English.
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2002; 2002US-0377071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%;
75.0%;
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Best Local Similarity 75.v.
Best Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selsted ME, Tran DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                Macaca mulatta
                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-2004.
                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   object.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiancy virus), sexually retracyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
                                                                                                                Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
                                                                                                                                                                                                                                                                                     /note= "Linked to amino acid at position 18 to form a cyclic structure"
3..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Linked to amino acid at position 1 to form a cyclic structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases. Vaginosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; DB 6;
Pred. No. 0.014;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hong TB;
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Gaps

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Search completed: October 26, 2004, 15:34:54

Job time : 116 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		!	Appl	Appli	Appl	Appl	Appl	Appl	Appl	4	Appli	Appl	Appl	Appl	Appl
		. !	28,	7	14,	28,	32	32,	30		-1	12,	13	24,	30,
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			S-10-060-102-28	8-10-427-715-2	S-10-427-715-14	S-10-721-839-28	8-10-060-102-33	S-10-721-839-32	S-10-060-102-3(S-10-313-994-1	S-10-427-715-1	S-10-427-715-12	S-10-427-715-13	S-10-427-715-24	US-10-721-839-30
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	5		116	116	116	116	103	103	101	101	101	101	101	101	101
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Sequence 29, Appl Sequence 5, Appli Sequence 6, Appli Sequence 9, Appli Sequence 27, Appl	equence 1, equence 27 equence 23 equence 31, equence 31, quence 53, equence 2,	34,00	7, 120 20 17 31 9,	Sequence 28, Appl Sequence 37, Appl Sequence 38, Appl Sequence 39, Appl Sequence 21, Appl
15 US-10-427-715 14 US-10-141-645 14 US-10-141-645 14 US-10-313-994 14 US-10-060-102	US-10-141-645 US-10-421-839 US-10-427-715 US-10-060-102 US-10-721-839 US-99-917-340- US-10-141-645 US-10-141-645	15 US-10-427 15 US-10-427 15 US-10-427 15 US-10-721 14 US-10-141 14 US-10-141 15 US-10-1427	14 US 10-141-6 15 US -10-427-7 15 US -10-427-7 15 US -10-427-7 15 US -10-141-6 14 US -10-141-6	15 15 15 15 15
14 100 86.2 1 15 93 80.2 1 16 93 80.2 1 17 91 78.4 1 18 90 77.6 1	20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			41 74 63.8 1 42 73 62.9 1 43 73 62.9 1 44 73 62.9 1 45 73 62.9 9

ALIGNMENTS

▼ .	060-102-28	Sequence 28, Application US/10060102	Publication No. US20030022829A1	GENERAL INFORMATION:	LICANT: MAURY, WENDY		LICANT: ROLLER, RICHARD		-		TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS	TITLE OF INVENTION: CATHELICIDINS	FILE REFERENCE: IOWA:035US	CURRENT APPLICATION NUMBER: US/10/060,102	CURRENT FILING DATE: 2002-02-22	PRIOR APPLICATION NUMBER: 60/309,368	PRIOR FILING DATE: 2001-08-01	PRIOR APPLICATION NUMBER: 60/265,270	PRIOR FILING DATE: 2001-01-30	NUMBER OF SEQ ID NOS: 32	SOFTWARE: Patentin Ver. 2.1	ID NO 28	NGTH: 18	PE: PRT	ORGANISM: Artificial Sequence	ATURE:	OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
KEGOLT. I	US-10-060-102-28	; Sequence 2	, Publication	GENERAL IN	; APPLICANT:	; APPLICANT:	, APPLICANT	, APPLICANT:	; APPLICANT:	; APPLICANT:	; TITLE OF	: TITLE OF :	; FILE REFE	; CURRENT A	; CURRENT F.	; PRIOR APPI	; PRIOR FIL	; PRIOR APPI	, PRIOR FIL	; NUMBER OF	; SOFTWARE:	SEQ ID NO 28	; CLENGTH: 18	; TYPE: PRT	, ORGANISM	; FEATURE:) OTHER INFORM ; OTHER INFORM ; TS-10-060-102-28

AND MAMMALI!

1 GFCRCICTRGFCRCICTR 18

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Query Match
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels (

.. 0

Gaps

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1 GFCRCICTRGFCRCICTR 18

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US-10-427-715-2
Sequence 2, Application US/10427715
Sequence 2, Application US/10427715
Publication VS-10040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE PEPRENCE: 66778-302 (UG5754)
CURRENT APLICATION NUMBER: US/10/427,715
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: synthetic construct US-10-427-715-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-10-427-715-14 / Sequence 14-Application US/10427715 Sequence 14-Application US/10427715 Publication No. US20040014669A1 GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/10721839
Publication No. US20040086535A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Macaca mulatta
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US-10-721-839-28
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APPLICANT: Train, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
FILE REFERENCE: 66778-302 (UC5754)
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0

.. 0 100.0%; Score 116; DB 15; Length 18; 100.0%; Pred. No. 1e-06; tive 0; Mismatches 0; Indels 0

; 0

Gaps

FAGGE 2

***PLICANT: "MAURY, WENDY

***PLICANT: STAPLETON, JACK

***PAPLICANT: ROLLER, RICHARD

***APPLICANT: ROLLER, RICHARD

***APPLICANT: ROLLER, MARK

***APPLICANT: ROLLER, MARK

***APPLICANT: NOVEL NIVERIA MATIVIRIA ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI!

***TITLE OF INVENTION: CATHELICIDINS

***PLICANT: TACK, BRIAN

***TITLE OF INVENTION: CATHELICIDINS

***PLICANT: NOVEL NIVER: US/10/721,839

***CURRENT FILING DATE: 2003-01-25

***PRIOR FILING DATE: 2003-02-22

***PRIOR FILING DATE: 2001-03-01

***PRIOR FILING DATE: 2001-03-01 ö Gaps OTHER INFORMATION: Description of Artificial Sequence: Synthetic in OTHER INFORMATION: Peptide US-10-721-839-28 ô Length 18; Indels 100.0%; Score 116; DB 15; 100.0%; Pred. No. 1e-06; iive 0; Mismatches 0; ; 0 1 GFCRCICTRGFCRCICTR 18 GPCRCICTRGFCRCICTR 18 TYPE: PRT ORGANISM: Artificial Sequence 18; Conservative Query Match Best Local Similarity Matches 18; Conserv ਨੇ d

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Gaps

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Indels

Length 18;

RESULT 5 US-10-060-102-32

Sequence 32, Application US/10060102

Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STANKI, MARK
APPLICANT: STANKI, MARK
APPLICANT: TACK, ERIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWALI!

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWALI!

TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICATION NUMBER: US/10/660,102
CURRENT PAPLICATION NUMBER: 60/2022
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 32
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 2.1
SEQ ID NO 32
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 2.1
SEQ ID NO 32
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2
INSTRUMENT BATENTING DATE: 201-30
NUMBER OF SEQ ID NOS: 3.2 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: Peptide US-10-060-102-32 88.8%; Score 103; DB 14; Length 18; 88.9%; Pred. No. 2.9e-05; Live 0; Mismatches 2; Indels TYPE: PRT ORGANISM: Artificial Sequence Query Match
Best Local Similarity 88.9
Matches 16; Conservative

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Gaps

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1 GFCRCICTRGFCRCICTR 18

Gaps

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USEQUENCE 1, Application US/10313994
; Sequence 1, Application US/10313994
; Publication No. US20030162718A1
; FERREAL INFORMATION;
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Vang, Van
; APPLICANT: Wall of the Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; TILE REPRENCE: P-UC 3095
; TILE OF INVENTION: ANTIMER: US/10/313,994
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR APPLICATION NUMBER: US/09/309,487
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE PATENT USE: 2.0
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 1, Application US/10427715 |
| Sequence 1, Application US/10427715 |
| Publication No. US20040014669A1 |
| Publication No. US20040014669A1 |
| Publication No. US20040014669A1 |
| APPLICANT: FIRSH, Michael E. |
| APPLICANT: Tran, Dat Q. |
| TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| TITLE OF INVENTION: Thereof, and Methods of Use |
| PRIOR PELING DATE: 2003-04-30 |
| PRIOR PELING DATE: 2002-04-30 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 18
                                                                                                                                                            Query Match 87.1%; Score 101; DB 14; Length 18; Best Local Similarity 83.3%; Pred. No. 4.8e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Macaca mulatta
                                                                                  US-10-060-102-30
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US-10-313-994-1
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LENGTH: 18
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                                                                                               RESULT 6
US-10-721-839-32
IS-10-721-839-32
IS-20-721-839-32
IS-20-721-839-32
IS-20-721-839-32
IS-20-721-839-32
IS-20-721-839-32
IS-20-721-839-32
IS-20-721-839-32
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IS-20-721-839-32
IS-20-721-839
IS-20-721-830
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| Sequence 30. Application US/10060102
| CENERAL INFORMATION:
| CENERAL INFORMATION:
| APPLICANT: MAURY, WENDY
| APPLICANT: STIAKI, MARK
| APPLICANT: STIAKI, MARK
| APPLICANT: STIAKI, MARK
| APPLICANT: TACK, BRIAN
| TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
| TITLE OF INVENTION: CATHELICIDINS
| TITLE OF INVENTION WIMBER: 60/202
| PRIOR FILING DATE: 2001-08-01
| PRIOR FILING DATE: 2001-08-01
| PRIOR FILING DATE: 2001-01-30
| NUMBER OF SEQ ID NOS: 32
| SOUTRARE PARENTED TOWN OF SEQ ID NOS: 32
| SEQ ID NO 30
| LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFCRCICTRGFCRCICTR 18
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1 GICRGICTRGFCRCICGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Gaps

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1 GFCRCLCRRGVCRCICTR 18

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APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 65778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR PILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARR: PARTSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: synthetic construct US-10-427-715-24
Sequence 24, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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0
                                                                                                                                      APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: ADDICACL and Methods of Use
FILE REFERENCE: 66778-302 (UG554)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PELING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/10427715
Publication No. US20040014669A1
FUBLICATION No. US20040014669A1
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat O.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 66778-302 (UGS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.1%; Score 101; DB 15; Length 18; Best Local Similarity 83.3%; Pred. No. 4.8e-05; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.1%; Score 101; DB 15; Best Local Similarity 83.3%; Pred. No. 4.8e-05; Matches 15; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-427-715-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic construct
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LOCATION: 18
COTHER INFORMATION: at the C terminus
US-10-427-715-13
                                     S-10-427-715-12
Sequence 12, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
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US-10-721-839-30
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Length 18;
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               2; Indels
Score 101; DB 15;
Pred. No. 4.8e-05;
               0; Mismatches
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US-10-141-645-6

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Query Match 80.2%; Score 93; DB 14; Length 18
Best Local Similarity 77.8%; Pred. No. 0.00038;
Matches 14; Conservative 1; Mismatches 3; Indels
Sequence (Application US/10141645)
Publication No. US20030144184A1
GENERAL INFORMATION
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Arexader Cole
CURRENT FILE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPREBUGE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141.645
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
FRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NO SEQ ID NOS: 125
MUNDER PROSTARE: FastSSQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic variant US-10-141-645-6
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ORGANISM: Artificial Sequence
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                                                      US-10-427-715-29
Sequence 29, Application US/10427715
Sequence 29, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE OF INVENTION: Thereof, and Methods of Use
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT PILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOUTHMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 18
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86.2%; Score 100; DB 15; Length 18;

Best Local Similarity 93.8%; Pred. No. 6.2e-05;

Matches 15; Conservative 0; Mismatches 1; Indels
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APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

ITILE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

FILE REFERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: 60/284, 855

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 125

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO

LENGTH: 18
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ORGANISM: Artificial Sequence
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US-10-141-645-5
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Gaps . 0

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Squence 9, Application US/10313994
Squence 9, Application US/10313994
Squence 9, Application No. US20030162718A1
GENERAL INPORATION:
APPLICANT: Scletcd, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Van, Jun
APPLICANT: Oucliette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/10/313,994
CURRENT FILING DATE: 2002-12-05
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 81.2%; Pred. No. 0.00063;
Matches 13; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Sequence 27, Application US/10060102; Publication No. US20030022829A1; GENERAL INFORMATION:
1 GFCRCICTRGFCRCICTR 18
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ORGANISM: Macaca mulatta
US-10-313-994-9
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US-10-060-102-27
                                                                                                                                                             US-10-313-994-9
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LENGTH: 18
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RESULT 16

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GENERAL INFORMATION:
APPLICANT: MAURY WENDY
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, DACK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION NUMBER: US/10/721,839
CURRENT APPLICATION NUMBER: US/10/660,102
FRICE PRICATION NUMBER: 60/309,368
FRICE PLING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR PLING DATE: 2001-08-01
PRIOR PLING DATE: 2001-08-01
SRICH PLING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 27
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Pred. No. 0.00081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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US-427-115-23
Sequence 23, Application US/10427715
Sequence 23, Application US/10427715
Sequence 23, Application US/10427715
Sequence 23, Application No. US20040014669A1
SEMERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Dat Q.
TITLE OF INVENTION: Dat Q.
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 66778-302 (UC5754)
CURRENT PRILING DATE: 2003-04-30
RICHARD APPLICATION NUMBER: US 60/377,071
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOUTHARD: EASTSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
Publication No. US20040086535A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 14; Conserva
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 18
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     APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: ROLLER, RICHARD
APPLICANT: ROLLER, RICHARD
APPLICANT: ACENARY
APPLICANT: TACK, BRIAN
ITILE OF INVENTION: CATHELICIDINS
ITILE OF INVENTION: CATHELICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR PELING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 27
LENGTH: 18
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-27
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Publication No. US20030144184A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral
APPLICANT: Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERBENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-05
PRIOR PHLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Matches 14; Conservative
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ORGANISM: Homo sapiens
US-10-141-645-1
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LENGTH: 18
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RESULT 22

RESULT 20 US-10-721-839-27 Sequence 27, Application US/10721839

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75.0%; Score 87; DB 9; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 1; Indels
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Sequence 2, Application US/10141645
PUblication No. US20030144184A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Tereas Hong
APPLICANT: Tereas Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PR
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Pred. No. 0.0018;
Best Local Similarity 72.2%; Pred. No. 0.0014;
Matches 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Murphy, Christopher J. APPLICANT: Marphy, Christopher J. APPLICANT: McAnulty, Jonathan F. APPLICANT: McAnulty, Jonathan F. APPLICANT: McAnulty, Jonathan F. TILLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468 US/09/917,340 CURRENT APPLICATION NUMBER: 05/21,632 PRIOR APPLICATION NUMBER: 60/221,632 PRIOR APPLICATION NUMBER: 60/249,602 PRIOR APPLICATION NUMBER: 60/249,602 PRIOR APPLICATION NUMBER: 60/299,932 PRIOR FILING DATE: 2001-01-17 PRIOR FILING DATE: 2001-05-15 NUMBER: OF SEQ ID NOS: 96 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: synthetic variant US-10-141-645-2
                                                                                                                                                                                                                                                                                                                                  US-09-917-340-53
; Sequence 53, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
                                                                                                            1 GFCRCICTRGFCRCICTR 18
                                                                                                                                                           75.0%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-917-340-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 53
LENGTH: 18
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       Sequence 31, Application US/10060102
| Sequence 31, Application US/2003022829A1
| Sequence 31, Application No. US2003022829A1
| GENERAL INFORMATION:
| APPLICANT: STAPLICANT: WENDY
| APPLICANT: STAPLICANT: ROLLER, RICHARD
| APPLICANT: ROLLER, RICHARD
| APPLICANT: MCRAY, PAUL B.
| APPLICANT: MCRAY, PAUL B.
| APPLICANT: ACK, BRIAN
| TITLE OF INVENTION: OTTHELICIDINS
| TITLE OF INVENTION: CATHELICIDINS
| TITLE OF INVENTION: CATHELICIDINS
| FILE REFERENCE: IOWA:035US
| CURRENT APPLICATION NUMBER: 60/309,368
| PRIOR PLING DATE: 2001-08-01
| PRIOR FILING DATE: 2001-08-01
| PRIOR FILING DATE: 2001-01-30
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 31
| LENGTH: 18
| LENGTH: 18
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| Publication No. US20040086535A1
| Sequence 31, Application US/20040086535A1
| GENERAL INFORMATION:
| APPLICANT: WAUNY, WENDY
| APPLICANT: STARETON, JACK
| APPLICANT: STINKI, MAKK
| APPLICANT: BILEN, RICHARD
| APPLICANT: ACLER, RICHARD
| APPLICANT: ACLER, RICHARD
| APPLICANT: MCKAY, PAUL B.
| TITLE OF INVENTION: CAPHELICIDINS
| TITLE OF INVENTION: CAPHELICIDINS
| TITLE OF INVENTION: CAPHELICATION NUMBER: US/10/721,839
| CURRENT APPLICATION NUMBER: US/10/060,102
| PRIOR PRIING DATE: 2003-11-25
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| WUMBER OF SEQ ID NOS: 32
| SEQ ID NO 31
| LEASTH. 18
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US-10-721-839-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Antidicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antidicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use.
FILE REFERENCE: 66778-302 (UCS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 15; Length 18;
Pred. No. 0.0023;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: synthetic construct US-10-427-715-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: AMIDATION
1 LOCATION: 18
1 LOCATION: 3
1 OTHER INFORMATION: at the C terminus
US-10-427-715-16
                                                                                                                  US-10-427-715-15
; Sequence 15, Application US/10427715
; Publication No. US20040014669A1
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  1 GFCRCICTRGFCRCICTR
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                          APPLICANT: MACRY, WENDY
APPLICANT: STABLETON, JACK
APPLICANT: STABLETON, JACK
APPLICANT: STINSKI, MAKK
APPLICANT: STINSKI, MAKK
APPLICANT: STINSKI, MAKK
APPLICANT: STINSKI, MAKK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: CAPITALICIDINS
TITLE OF INVENTION: CAPITALICIDINS
TITLE OF INVENTION: CAPITALICIDINS
TITLE OF INVENTION: CAPITALICIDINS
TITLE OF STERNOR: 100A: 03-22
CURRENT APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 29
LENGTH: 18
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Gaps
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Bublication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael B.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US 60/377,715

CURRENT APPLICATION NUMBER: US 60/377,71

PRIOR APPLICATION NUMBER: US 60/377,71

FRIOR APPLICATION NUMBER: US 60/377,71

FRIOR APPLICATION NUMBER: US 60/377,71

CURRENT FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

LENGTH: 18

LENGTH: 18

TYPE: PRIOR MAGCA mulatta
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4; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                US-10-060-102-29; Sequence 29, Application US/10060102; Sequence 29, Eublication No. US20030022829A1; GENERAL INFORMATION:
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                                         1 GPCRCICTRGFCRCICTR 18
                                                                            1 GICRCICGKGICRCICGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Matches 12; Conservative
  13; Conservative
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Matches 12; Conserva
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                                      Gaps
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                               US-10-141-845-9

Sequence 4, Application US/10141645

Publication No. US20030144184A1

GENERAL INFORMATION

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

FILE REFERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2002-05-06

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEC ID NOS: 125

SEOTHARE: FastSEC for Windows Version 4.0

LENGTH: 18
Best Local Similarity 72.2%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 5;
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, OTHER INFORMATION: synthetic construct
US-10-427-715-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: synthetic variant
                                                                                                                                                                            1 GICRCYCGRGICRCICGR 18
                                                                                                                         1 GFCRCICTRGFCRCICTR 18
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ORGANISM: Artificial Sequence
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                                                                                                                             Sequence 29, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLICANT: MARK

APPLICANT: TACK: RAIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWMALT

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAWMALT

TITLE OF INVENTION: NOVEL ANTIVIRAL SOURCESSED SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-721-839-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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Publication No. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Teresa Hong

ITILE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

TITLE OF INVENTION: Antimicrobial Peptides

FILE REPERENCE: UCLA-001CIP

CURRENT FILING DATE: 2002-05-06

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

74.1%; Score 86; DB 15;
Best Local Similarity 66.7%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCICTRGFCRCICTR 18
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                                                                         RESULT 30
US-10-721-839-29
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73.3%; Score 85; DB 14; Length 18;

Query Match

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US-10-427-715-17
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TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Methods of Use
TITLE OF INVENTION: Thereof, and Methods of Use
TITLE OF INVENTION: Thereof, and Methods of Use
TITLE OF INVENTION NUMBER: US/10/427,715
CURRENT PILING DATE: 2003-04-30
PRICR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.6%; Score 83; DB 15; Length 18; Best Local Similarity 72.2%; Pred. No. 0.0049; Matches 13; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.6%; Score 83; DB 14; Length 18; Best Local Similarity 72.2%; Pred. No. 0.0049; Matches 13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                       GENERAL INFORMATION: US/10141645

PUBLICATION NO. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Alexander Cole

CONSTRUM APPLICANTON: Antimicrobial Peptides

FILE REFREENCE: UGLA-001CIP

CURRENT APPLICATION NUMBER: 00/284,855

PRIOR FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: Unassigned

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOFTWARE FASEEQ for Windows Version 4.0

SEGOLD NO 7
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; OTHER INFORMATION: synthetic variant
US-10-141-645-7
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, Sequence 19, Application US/10427715
, Publication No. US/20040014669A1
, GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
1 GFCRCICTRGFCRCIC 16
                               1 GICRCLCRRGVCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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; Sequence 17, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selected, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; TITLE REFERENCE: 66778-302 (UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR PLING DATE: 2002-04-30
; NUMBER OF SEC ID NOS: 41
; SEQ ID NO 17
; SEQ ID NO 17
; LENGTH: 18
                                                                           GENERAL INCOMENTATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER: OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.6%; Score 83; DB 15; Length 18; Best Local Similarity 72.2%; Pred. No. 0.0049; Matches 13; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: synthetic construct US-10-427-715-20
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; OTHER INFORMATION: at the C terminus
US-10-427-715-17
Sequence 20, Application US/10427715; Publication No. US20040014669A1; GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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RESULT 38

1 GFCRALCRRGVCRAICTR 18

GENERAL INFORMATION:

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              Sequence 31, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT APPLICATION NUMBER: US 60/377,071
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
FENDINE: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.7%; Score 82; DB 15; Length 18; Best Local Similarity 75.0%; Pred. No. 0.0064; Matches 12; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-1U-11-045-8

US-1U-11-045-8

Publication No. US20030144184A1

GENERAL INFORMATION:

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANT: Teresa Hong

ITILE OF INVENTION: Retrocyclins - Antiviral and

ITILE OF INVENTION: Antimicrobial Peptides

TILE APPLICATION NUMBER: US/10/141,645

CURRENT APPLICATION NUMBER: 00/2-05-06

CURRENT FILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOUTWARE: SEQ ID NOS: 125

SEQ ID NO 8

LENGTH HORSE OF WINDOWS Version 4.0

SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

COTHER INFORMATION: synthetic construct
US-10-427-715-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: synthetic variant US-10-141-645-8
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US-10-427-715-31
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Sequence 9, Application US/10141645 Publication No. US20030144184A1

RESULT 40 US-10-141-645-9

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APPLICANT: Robert Lehrer
APPLICANT: Alan Wating
APPLICANT: Alan Wating
APPLICANT: Alan Wating
APPLICANT: Alexander Cole
I TITLE OF INVENTION: Retrocyclins - Antiviral and
I TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERRNCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PLING DATE: 2002-06-6
FRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/20-66
PRIOR FILING DATE: 2002-04-18
FRIOR APPLICATION NUMBER: Unasigned
PRIOR FILING DATE: 2002-04-18
FRIOR APPLICATION NUMBER: Unasigned
FRIOR APPLICATION NUMBER: Unasigned
FRIOR APPLICATION NUMBER: 00/20-14-18
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2004, 15:13:56 ; Search time 128.5 Seconds (without alignments) 80.597 Million cell updates/sec Run on:

US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	E	Q9tu01 macaca mula	Q6p8t4 mus musculu	Q8ch20 mus musculu	Q9d9i2 mus musculu	Aah61079 mus muscu	mus mu	Q949g1 oryza sativ	Q8vj20 mycobacteri		O96282 plasmodium		Q7seq2 neurospora						Q75nz5 chlamydomon	Bad13491 chlamydom	Bad13492 chlamydom	Q75n88 homo sapien	Bad16738 homo sapi	Q75n87 homo sapien				σ			Q7qbv4 anopheles g
SUMMARIES	ID	P82270	Q9TU01	Q6P8T4	Q8CH20	Q9D9I2	AAH61079	Q9D4K2	Q949G1	Q8VJ20	Q9BLJ1	096282	YO70 NPVAC	Q7SEQ2	Q9NRB6	Q2204B	Q95QY1	Q18238	017641	Q75NZ5	BAD13491	BAD13492	Q75N88	BAD16738	Q75N87	BAD16739	075770	Q94UZ6	Q6RY99	AAR24072	Q9PYQ3	Q7QBV4
	DB	7	7	7	N	0	~	N	7	N	N	N	Н	N	N	~	N	N	~	7	7	N	N	~	7	0	7	~	01	N	0	7
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	% Query Match				50.9	50.9	50.9	50.9	50.9	48.7	48.3	47.0	46.6	46.6	46.1	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.3		•	45.3		44.8
	Score	64	64	59	59	59	59	59	59	56.5	26	54.5	54	54	53.5	53	53	23	53	53	53	23	23	53	53	23	52.5	52.5	52.5	52.5	52	25
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Gaps ô

Query Match
Best Local Similarity 83.3%; Pred. No. 0.35;
Matches 10; Conservative 1; Mismatches 1; Indels

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Q8MZ55 Q7PRP5 Q9U123 Q9U123 Q6CG37 1BB PHAAU Q6ZĞ82 Q91ZH6 Q7PN9 VEGC_MOUSE Q91ZE3 BAC31172 VEGC_HUMAN	AAH63685
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ALIGNMENTS

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1 E				sequence update) annotation update)	
DE	Ö	ounit A		(RTD-1)	
E	Name=RTD1A;				
SO	Macaca mulatta (Rhesus macaque)	us macac	que).		
ဗ	Metazoa;	Chordata;			; Euteleostomi;
ဗ	œ :	Primates;	s; Catarrhini;	ini; Cercopithecidae;	hecidae;
S S	Cercopithecinae; Macaca	aca.			
٠ د د د	11)				
R.P.	UENCE FROM N.A.,	SEQUENCE OF	E OF 65-73,	AND MASS	SPECTROMETRY.
RC	TISSUE=Bone marrow, a	and Leu			
ξĶ	MEDLINE=99453140; PubMed=10521339;	OMed=10!	1339		
Z.	Tang YQ., Yuan J.,	Oesapay G.,	y G., Oesapay	pay K., Tran D.,	D., Miller C.J.,
E E	Ouellette A.J., Selsted M.E.;	Ced M.E	,	-	
H E	"A Cyclic Antimicrobi	tai Pepi	croblal Peptide Produced in Translet al	ced in Primare	e neukocytes by the
Ϋ́	Science 286:498-502(1	1999)	rpiia-perei		
ខ្ល	-!- FUNCTION: Microbicidal		activity a	gainst Gram-po	activity against Gram-positive bacteria
ပ္ပ	S.aureus and L.monocytogenes, Gram-negative bacteria S.tyr		genes, Gra	m-negative ba	cteria S.typhimurium
ខ្ល	and E.coli ML35	and fung	gi C.albic	ans and C.neo	`
ပ္ပ	-!- SUBUNIT: Heterodi	imer of	subunit A	and subunit	B linked by a
ပ္ပင္မ	distilld bond at	position	on be rorm	d bond at position be forming a cyclic KiD-1.	KID-1.
ع ڊ	41000E	ייים ביון	indition i	מהי ליסיה לייסית	
ع د	-I- DEVELOPMENTAL STAGE: Expression and peptide	AGR. Ext	nonocyces.	nd peptide	accumulation starts
ָ ט		100	ansamilogerto mesolono osi		
ع د	-I- MASS SPECTROMETRY: MW=2082.0: METHOD=MALDI	V: MW=2(CE MYCLOPC 282.0: MET	HOD=MALDI.	
ខ្លួ	MISCE	ne deter	rmined pI of	of this protein	in is greater than
S	12.		•	•	
ខ	MILARITY:	ags to the	he	corticostatin/defensin	sin family.
띥	AF191100;	AAF04389.1;	;		
띪	EMBL; AF191102; AAF04	4391.1;			
DR		,			
E I	GO; GO:0050832; P:def	fense re	P:defense response to	fungi; IEA.	
8		noblotic	P:xenoblotic metabolism;	sm; IEA.	
8 G	InterPro; IPR002366; Detensin proper	Detens	in propep.		
Z 5	Pram; Pruos/9; Derensin Dropep; I.	sin proj	pep; I. Mae Sign		
5 6	CICINIT.		DOTENTIAL.	·	
7 E	15	2 4	1	į	
·	ייני	73	THETA DE		SUBUNIT A.
ı E	P 7.4	76	REMOVED	REMOVED IN MATURE FORM.	
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Basic protein CKT1R3.
Name=4931420D14Rik; Synonyms=Ckt1r3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9D912;
01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 CRCCCYCRCCRCCSR
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Best Local Similarity
Matches 9; Conservat
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8CH20
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Strumberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Baher N.K.,

Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Baher N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McZwan P.J., McKernan K.J., Maher J.A., Gunazane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
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Demidefensin 2.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Zhao C., Nguyen T., Lehrer R.I.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1041:57; AAR07924.1;
GO; GO:0006952; P:defense response; IEA.
InterPro; IPR002366; Defensin_propep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00879; Defensin proper; 1. SEQUENCE 76 AA; 8212 MW; 1EB307932A031826 CRC64;
                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                            76 AA
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                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
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                                          RCICTRGFCRCI 15
                                                                                                    65 RCICTRGFCRLL 76
                                                                                                                                                                                                                                                            PRELIMINARY;
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Mus musculus (Mouse)
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01-MAY-2000
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Q6P8T4;
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В

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Gaps
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700065105 product:hypothetical Cysteine-rich region
containing protein, full insert sequence.
Name=4931420D14Rik;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                Length 168;
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Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AAH61079.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 18947 MW; BOOFD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                50.9%; Score 59; DB 2; 56.2%; Pred. No. 3; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%; Sco. No. 5, 56.2%; Pred. No. 5,
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A MEDLINE=2288257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rokaran P.J., McKernan K.J., Malek J.A., Gunaratne P.H., ARA S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulko B., Kethards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulko B., Kethards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulko B., Kethards S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schner A., Schein J.E., Schnerch A., Sc
                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BCO61079; AAH61079.1; -. Hypothetical.protein. Hypothetical.protein. SEQUENCE 168 AA; 18947 MW; BO0FD3D27B9BF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sci. U.S.A. 99:16899-16903(2002).
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Hypothetical protein.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.2'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad.
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                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                     TISSUE=Testis;
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09D4K2
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0
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRALM-ESTBL/617 IISBUE=Testis;
STRALM-ESTBL/617 IISBUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Testis;
MEDILINE=20499374; PubNed=11042159;
MEDILINE=20499374; PubNed=11042159;
Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C5-FBLG-40; TISSUE=Testis; STRAIN-C5-FBLG-40; TISSUE=Testis; Akimura T., Arai A., Aono H., Ardachi J., Aizawa T., Akahira S., Akimura T., Pukuda S., Fukunishi Y., Furuno M., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanza A., Hayatsu N., Hiramoto K., Hiracka T., Kato H., Kawai J., Kojima Y., Tohno H., Kouda M., Koya S., Kurihara C., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sakai C., Sakai C., Saloo H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Soqabe Y., Suzuki H., Tagawa M., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Miramatsu M., Hayashizaki Y., Miramatsu M., Hayashizaki Y., Miramatsu M., Hayashizaki Y., Miramatsu M., Hayashizaki Y., Miramatsu M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Itasuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Pujiwake S., Inoue K., Togawa M., Dara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated Sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida F
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .l protein.
168 AA; 18931 MW; 7AZBD279612A5E94 CRC64;
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(TremBlrel. 27, Last sequence update)
(TremBlrel. 27, Last annotation update)
              SEQUENCE FROM N.A.
STRAIN-CSPEL/G6, TISSUE-Testis,
MEDLIADE-21085660; PubMed-11217851,
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AKO06892; BAB24782.1; -..
MGD; MGI:1913992; 4931420D14Rik.
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Best Local Similarity که ۱۵۰۰
Best Local 9, Conservative
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AAH61079;
14-APR-2004 (
14-APR-2004 (
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AAH61079
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4931420D14 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                ;
0
50.9%; Score 59; DB 2; Length 168; 56.2%; Pred. No. 3;
                                                                Indels
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STRAIN=CS7BL/6J; TISSUB=Testis;
MEDLINE=9927923; Pubmed=10349636;
Carninci P., Hayashizaki X.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
Fraser C.M.,
                                                                                                                                                                                                      MEDLINE-21329048; PubMed=11435398; Mayer K., Wurphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., Bevan M., Bancroft I.; an odeweerd A.M., Tingey S.V., Mewes H.W., "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis thaliana.";
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 59; DB 2; Length 274; 66.7%; Pred. No. 4.5; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 11:1167-1174(2001).

EMBL; AJ307662; CAG39030.1; -.

Gramene; Q949G1; -.

Hypothetical protein.

SEQUENCE 274 AA; 28657 WW; AB547D9BD5470AEI CRC64;
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Last annotation update)
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J. Bacteriol. 184:5479-5490(2002).
EMBL; AE007152; AAK47795.1; -.
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01-MAR-2002 (TremBirel. 20,
Hypothetical protein MT3454.
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Matches 10; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                            NCBI_TaxID=4530;
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakwar T., Bono H., Carminoi P., Pukuda S., Fukunishi Y., Furuno M.,
Hanaqaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Koya S., Hiraoka T., Kato H.,
A Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sano H., Yanamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AKO16467; BAB30253.1,
                                                                                                                               SEQUENCE FROM N.A.
STRANIE-STBL/61/ TISSUB=Testis,
The FANTOM CONSORtium.
The RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
60,770 full-length cDNAs.";
Nature 420:553-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes:";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20530913; PubMed=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Katsunai T., Tashiro H., Itoh M., Kucuno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M., Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yanada K., Togawa Y., Izawa M., Ohara E., Watsunai K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Cawa K., Tanaka T., Matsuura S., Kawai J., Rishikawi T., Sakikawa T., Matsuura S., Kawai J., Rishikawi B., Inoue Y., Kira A., Hayashizaki Y., Rishikawi Saquence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001),
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SEQUENCE 173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CRCICTRGFCRCICTR 18
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Matches 9; Conservative
RIKEN FANTOM Consortium;
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0949G1
1D 0949G
AC 0949G1
DT 01-D
DT 01-D
DT 01-D
GN Name
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163 AA

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Gaps

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;
                                    DB 2; Length 163;
                                                            Indels
Hypothetical protein.
SEQUENCE 163 AA; 18621 MW; BSE62AB951B2AC3C CRC64;
                                                           2;
                                    Score 56.5; DB
Pred. No. 6;
3; Mismatches
                                                                                                                                                                   937 AA.
                                                                                                                                                                   PRT;
                                                                                                         137 CRHVCTRSGYCRLVC 151
                                                                                   3 CRCICTR-GFCRCIC 16
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                  Q9BLJ1,
Q9BLJ1;
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Q9BLJ1
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C15ERIPDM.
Name=C15ERIPDM;
Oryza Sativa (Rice).

PRELIMINARY;

Q949G1 Q949G1;

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46.6%; Score 54;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Y070_NPVAC
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Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
                                                                                                                                          Name=Ci-metal;
Chona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes that are expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                             MEDLINE=21347414; PubMed=11455433;

A Nakayama A., Satou Y., Satou Y., Satou Y., Satou Y., Satou Y., Satou M., Satou Y., Satou Y., Satou M., Satou J., Satou M., Satou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PFB0950w.
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Ci-MRT-1.
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                                                                                                                                                                                                                                                                                                                            MEDLINE=22255705; PubMed=12368864; MEDLINE=22255705; PubMed=12368864; MEDLINE=22255705; PubMed=12368864; Medicar M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Perrea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Wefadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Davis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O., Fraesr C.M., Adams M.D., Venter J.C., Hoffman S.L., "Chromosome 2 sequence of the human malaria parasite Plasmodium falcibarum.";
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Ayres M.D., Howard S.C., Kurlo J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus.";
Virology 202:586-605(1994).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
Hypothetical 34,4 Kba protein in LEF3-IAP2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dabNa viruses, no RNA stage; Baculoviridae;
NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

47.0%; Score 54.5; DB 2; Length 307;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 2; Indels
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Nature 419:498-511(2002).
Nature 419:498-511(2002).
PIRI, AE001428; AAC71979.2; -.
PIRI, E71602; E71602.
InterPro; IPR001368; TNFR c6.
PROSITE; PS00652; TNFR NGFR_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000519; P_trefoil.
Hypothetical protein.
SEQUENCE 290 AA; 34408 MW; CA78BA9C8B5AB997 CRC64;
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                                                                                                                                                                                                                Science 282:1126-1132(1998).
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DB 1; Length 290;

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Chesi M., Brents L.A., Ely S.A., Bais C., Mesri E.A., Robbiani D., Kuchl W.M., Bergsagel P.L.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF238374; AAF97749.1; -.
GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worner, Carrier, 101878; CE03592.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR006081; Defensin alpha.
InterPro; IPR006009; EGF like.
InterPro; IPR001007; VWF C.
PROSITE; PS001089; 4Fe4S FERREDOXIN; UNKNOWN_1.
PROSITE; PS000269; DEFENSIN; UNKNOWN_1.
PROSITE; PS00022; EGF 1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                  164 AA.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                       75 GLCVCVCV---CVCVCT 88
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Query Match

Best Local Similarity 50.vv,

Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=T01B7.8;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 164 AA; 1
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SEQUENCE
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ID Q9SQY1
AC Q9SQY1;
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0
                           Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariomycetidae, Sordariales; Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.6%; Score 54; DB 2; Length 991; 56.2%; Pred. No. 59; tive 0; Mismatches 7; Indels
                           4; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mutant fibroblast growth factor receptor 3 (Fragment).
                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                              991 AA
                         2; Mismatches
         Pred. No. 21;
                                                                                     218 FARCFCTNTMQCFCPRQGYKCECICRR 244
                                                             2 FCRCICT-----RGF-CRCICTR 18
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                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL, AABXO1000029; EAA35288.1; -.
INCEPERO, IPRO06209; EGF_like.
PROSITE; PSO0022; EGF_1.1
PROSITE; PSO1186; EGF_2; 1.
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     40.78;
       Best Local Similarity 40.73
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                         Predicted protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5141;
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                                                                                                                                                      RESULT 13
Q7SEQ2
ID Q7SEQ2;
AC Q7SEQ2;
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RESULT 14 Q9NRB6

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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                      3,
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                                             / Match 46.1%; Score 53.5; DB 2; Length 174; Local Similarity 47.1%; Pred. No. 15; 168 8; Conservative 2; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 2; Length 164;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sims M.A.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 256499; CAA91301.1; -.
PIR; T24272; T24272.
HSSP; P10968; 2CWG.
174 AA; 17810 MW; BC9917E34470B9EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16499 MW; C002D48D36C9FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
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us-10-009-317a-32.rup
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Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                      PERCENCE FROM N.A.

SEQUENCE FROM N.A.

Waterston R.;

National Conditions of the EMBL/GenBank/DDBJ databases.

EMBL; US8760; AAX31463.1; -...

EMBL; US8760; AAX31463.1; -...

EMBL; US8760; AAX31463.1; -...

EMBL; US8760; AAX31463.1; -...

R PIR, TILSE31.

TILSE41.

R POST TISE51.

R GO; GO: 000557; C: extracellular; IEA.

GO; GO: 000557; C: extracellular; IEA.

GO; GO: 000557; P: defense response; IEA.

GO; GO: 000557; P: response to pest/pathogen/parasite; IEA.

GO; GO: 000557; P: response to pest/pathogen/parasite; IEA.

R GO; GO: 000557; P: response to pest/pathogen/parasite; IEA.

R GO; GO: 000557; P: response to pest/pathogen/parasite; IEA.

R GO; GO: 000557; P: response to pest/pathogen/parasite; IEA.

R PROSITE; PS00190; 4FE45 FERREDOXIN; UNKNOWN_1.

PROSITE; PS001209; WFC_1; UNKNOWN_1.

PROSITE; PS01209; WFC_1; UNKNOWN_1.

R PROSITE; PS01209; WFC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 9; Indels
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Waterston R.;
Submitted (JAN-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; U55884, AAK68161.1;
HSSP; P10969; 1NGT.
Wormbep; C0466-7; CE27652.
InterPro; IPR00450; 4Fe4S, ferredoxin.
InterPro; IPR006091; DefenSin_alpha.
InterPro; IPR006091; WFC.
InterPro; IPR001099; VWFC.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNROWN_1.
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STRANDE Bristol N.S.
Anderson K., Chissos S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                               to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
Hypothetical protein C04G6.7.
ORFNames=C04G6.7;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                       Nhan M.;
Submitted (MAY-1996)
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STRAIN-Bristol N2;
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Q17641
ID Q17641
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
08-FNames=C04G6.10;
Caenorhabditis elegans.
Ebukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Best Local Similarity 50.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 9; Indels
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STRAIN=Bristol N2;
Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, U55854; AAK68158.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Anderson K./ Chissos S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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SEQUENCE FROM N.A.
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RESULT 17 Q18238

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Gaps

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Yoshioka S., Taniguchi F., Miura K., Inoue T., Yamano T., Fukuzawa H.; "A Novel Myb Transcription Factor LCR1 Regulates the CO2-Responsive Gene Cahl Encoding A Periplasmic Carbonic Anhydrase in Chlamydomonas reinhardtii.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Vobloka S., Taniguchi F., Miura K., Incue T., Yamano T., Fukuzawa H.;
Vobloka S., Taniguchi F., Miura K., Incue T., Yamano T., Fukuzawa H.;
"A Novel Myb Transcription Factor LCR1 Regulates the CO2-Responsive
Gene Cahl Encoding A Periplasmic Carbonic Anhydrase in Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RUCHONCE FROM N.A.

Kucho K., Yoshioka S., Taniguchi F., Ohyama K., Fukuzawa H.;

Kucho K., Yoshioka G., Taniguchi F., Ohyama K., Fukuzawa H.;

Figeracting elements and DNA-binding proteins involved in CO2-

Figeracting elements and DNA-binding proteins involved in CO2-

Figeracting elements in Chlamydomonas reinhardtii.";

Flant Physiol. 133:783-793 (2003).

EMBL; AB168089; BAD13491.1;

SEQUENCE 602 AA; 62736 MW; 3DD94253D5A792DO CRC64;
                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Ukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeae; Chlamydomonas.
NCBI_TaxID=3055;
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                                                                                                  01-APR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
LOW-CO2 inducible Myb transcription factor LCRI.
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01-APR-2004 (TrEMBLrel. 27, Last seq
01-APR-2004 (TrEMBLrel. 27, Last ann
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                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3055;
                                            BAD13491
BAD13491;
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BAD13492
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AC BAD13491
DT O1-2
DT O1-2
DT O1-3
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SEQUENCE FROM N.A.
SEQUENCE S., Taniguchi F., Miura K., Inoue T., Yamano T., Fukuzawa H.
"A Novel Myb Transcription Factor LCR1 Regulates the CO2-Responsive
Gene Cahl Encoding A Periplasmic Carbonic Anhydrase in Chlamydomonas
reinhardtii.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae; Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae; Chlamydomonas.
VCI_TaxID=3055;
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                                                                                                                                                                                              Score 53, DB 2; Length 197;
Pred. No. 20;
0; Mismatches 9; Indels
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PROSITE; PS00269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01022; EGF 1; UNKNOWN 1.
PROSITE; PS01208; VMFC_1; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 197 AA; 20596 MW; FB5F9457BFB9BBAD CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Low-CO2 inducible Myb transcription factor LCR1.
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                                                                                                                                                                                              / Match 45.7%;
Local Similarity 50.0%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         82 GGGGCCCRPRCCCCCRR
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SEQUENCE FROM N.A.
PubMed=14555782;
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SEQUENCE FROM N.A.
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Best Local S
Matches 9
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Q75NZ5
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Gaps
SEQUENCE FROM N.A.
Asamizu E., Miura K., Kucho K., Inoue Y., Fukuzawa H., Ohyama K.,
Nakamura Y., Tabata S.,
"Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii.";
DNA Res. 7:305-307(2000)
EMBL, AB168090, BAD13492.1;
EMBL, AB168090, BAD13492.1;
SEQUENCE 602 AA; 62736 MW; 3DD94253D5A792D0 CRC64;
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                                                                                                                                                                                                                                                               45.7%; Score 53; DB 2; Length 602; 75.0%; Pred. No. 51; 3; Indels ative 0; Mismatches 3; Indels
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         Matches
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Gaps

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471 CTRCQCRCICCR 482

ઠે d δ ö No 11 Journal Property Contains 2 GF-11 Contains 2 GF-12 Contains 2 GF-13 SEQUENCE FROM N.A. Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S., Ito E., Gaps Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606; Name=FBNI;

Momo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. ö Query Match
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels RESULT 23
BAD16738

TO SALE SALE PRELIMINARY; PRT; 1365 AA.

BAD16738,

DT 26-APR-2004 (TrEMBLrel. 27, Created)

DT 26-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 26-APR-2004 (TrEMBLrel. 27, Last annotation update)

DE FIDTILID 1.

GN FBNI.

GN FBNI.

CO Marmalia; Metazoa; Chordata; Craniata; Vertebrata; But oc Marmalia; Butheria; Primates; Catarrhini; Hominidae; HO OC Marmalia; Eutheria; Primates; Catarrhini; Hominidae; HO NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T.R.

RA Ito B.; O75N88; 05-UUL-2004 (TrEMBLrel. 27, Created) 05-UUL-2004 (TrEMBLrel. 27, Last sequence update) 05-UUL-2004 (TrEMBLrel. 27, Last annotation update) Fibrillin 1. 464 RCIPTPGSCRCECNK 478 4 RCICTRGFCRCICTR 18 PRELIMINARY; 075N8B RESULT 22 5N88 Sow was a supported to the support of the support o g ઠે

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RP SEQUENCE FROM N.A.

RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,

RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,

R. Lo B.;

Luc B.;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"3 Novel mutations of Fibrillin-1 and 10 single nucleotide polymorphisms of Fibrillin-3 in Marfan syndrome patients."; Submitted (AFR-2004) to the EMBL, AGENBAN/DDBJ databases. EMBL, 38177802; BAD16738.1; -. SEQUENCE 1365 AA; 147448 MW; ED83FB79C1B2BD48 CRC64;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fibrilin 1.
Name=FBN1;
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BAD16739;
26-APR-2004 (TrEMBLrel. 27, Created)
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464 RCIPTPGSCRCECNK 478
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BAD16739
ID BAD16
AC BAD16
DT 26-AP
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Matches
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Q75N87
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN Wistar; TISSUE-Hippocampus;
Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
Goballe S., Aunis D., Maitre M.;
"Cloning and characterization of a rat brain receptor that binds the
endogenous neuromodulator gamma-hydroxybutyrate.";
PASEB J. 0.0-0(2004).
EMBL; AV45593; AR24072.1; -
GO, GO:0004872; F:receptor activity; IEA.
InterPro: IPR011209; Ribosomal S14.
InterPro: IPR00935; Tetraspanin.
InterPro: IPR00935; Tetraspanin.
PEam; PF00335; Tetraspanin; I.
                                                                                                                                                                                                          Length 273;
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                                                                                                                                                                                                                                                        3; Indels
                                                                                          Aphasizhev R., Aphasizheva I., Simpson L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF411047; AALOS568 1; - SEQUENCE 273 AA; 31149 MW; 4C0321A819A9E564 CRC64;
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                                                                                                                                                                                                       45.3%; Score 52.5; DB 2;
50.0%; Pred. No. 30;
iive 2; Mismatches 3;
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PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
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50.0%; Pred. No. 52;
tive 2; Mismatches
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STRAIN=Wistar; TISSUE=Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gamma-hydroxybutyrate receptor.
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Best Local Similarity 50.vv
Best Local Similarity
6, Conservative
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  lizard Leishmania.
NCBI_TaxID=5689;
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AAR24072;
02-MAR-2004
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SEQUENCE
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110 AAR2

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                                                                                                                                                                                                   SEQUENCE FROM N.A.
Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Toki T., Yonesaka S.,
Ito E.,
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000023822 (Fragment).
Name=ENSANGG0000020032;
Anophales gambiae str. PEST.
ENSANGG000002003 Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera, Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TAXID=180454;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
28 kDa guide RNA binding protein.
Leishmania tarentolae (Sauroleishmania tarentolae).
Mitochondarion.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
                                                                                                           Eukaryoča, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                    "3 Novel mutations of Fibrillin-1 and 10 single nucleotide polymorphisms of Fibrillin-3 in Marfan syndrome patients."; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; ABT/7803; BAD16739.1; -. SEQUENCE 2871 AA; 312219 MW; C3D044A80321E082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 53; DB 2; Length 2871; 60.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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26-APR-2004 (TrEMBLrel. 27, Last sequence update)
25-APR-2004 (TrEMBLrel. 27, Last annotation update)
Fibrilin 1.
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EMBL, AAABO1008964; EAA43873.1; -.
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                     Homo sapiens (Human)
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                                                                                                                                                            NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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Gaps

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Another Sequencing Consortium;
Another Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an -- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/AAAB01008847; EAA06854.2; -.
InterPro; IPR000152; EGF_2:
InterPro; IPR000152; EGF_1ixe.
InterPro; IPR001919; Hyalin.
InterPro; IPR001791; Laminin_G.
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44 CVCVLGWCRCV 54
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Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P., Gobaille S., Aunis D., Maitre M.; "Cloning and characterization of a rat brain receptor that binds the endogenous neuromodulator gamma-hydroxybutyrate."; EMSEB J. 0:0-0(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgCP1494 (Fragment).
Name=agCd47401; ORFNames=ENSANGG0000012913;
Anopheles gambiae EPEN: PEST
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                            Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum granulovirus).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=9943-230; PubMed=10502508;

MEDLINE=9943-230; PubMed=10502508;

HayAkawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;

"Sequence analysis of the Xestia c-nigrum granulovirus genome.";

"Sequence analysis of the Xestia c-nigrum granulovirus genome.";

"YiroLogy 262:277-297(1999).

EMBL, AF162221; AAP6257.1;

SEQUENCE 66 AA; 7457 MW; DD814F5A3F0ABEIO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PREST:
Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAABO1008859; EAA07639.1; -.

NON TER 1
SEQÜENCE 146 AA; 16746 MW; 7D32BBAABE776F98 CRC64;
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0
                                                                                                                             DB 2; Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 44.8%; Score 52; DB 2; Length 66; Local Similarity 47.1%; Pred. No. 10; es 8; Conservative 1; Mismatches 8; Indels
                                                                                                                                                       5; Indels
                                                                                               512 AA; 56146 MW; 44DD12B937C40D60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  66 AA.
                                                                                                                          / Match
Local Similarity 50.0%; Pred. No. 52;
tes 8; Conservative 2; Mismatches
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                                                                                                                                                                                                            386 CVCVCVR-VCLCLCVR 400
                                                                                                                                                                                   3 CRCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                              Q9PYQ3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
ORF143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                      Name=ORF143;
                                                                                        Receptor.
SEQUENCE
                                                                                                                             Query Match
Best Local S:
Matches 8
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Matches
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                                                                                                                                                                                                                                                         RESULT 30
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Berkeley; Stapleton M., Brostein D., Hong L., Agbayani A., Carlson J., Chapleton M., Brostein D., Frise E., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Madopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.9%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 6; Indels
Score 52; DB 2; Length 146;
Pred. No. 20;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY113346; AAM29351.1; -. FlyBase; FBGN063249; BCDNA:GH14618. SEQUENCE 161 AA; 17659 MW; EB41C9D94274EE94 CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
1-WAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO000019046 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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MEDINE-95096014; PubMed=7798176;

X. RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 10-31, AND REVISIONS.

MEDINE-95096014; PubMed=7798176;

Li Y., Huang Q., Zhang S., Liu S., Qi C., Tang Y.;

Li Y., Huang Q., Zhang S., Liu S., Qi C., Tang Y.;

Tury contain inhibitor: chemical synchesis, refolding, and the crystallographic analysis of its complex with trypsin.";

C. Biochem. 16:18-25(1994).

"Biochem. 16:18-25(1994).

"Biochem. 16:18-25(1994).

"MISCELLANBOUS: Functionally this inhibitor is unusual in that it stoichiometrically inhibits trypsin in a molar ratio of 1:2.

"I MISCELLANBOUS: The specificities and functions of this superfamily of inhibitors depend not only on the active sites within the domains, but also upon the amino acid composition, and resulting molecular conformation, surrounding these regions.

"MEGELLANBOUS: Three isoinhibitors are also found whose amino ends differ slightly from that shown.

"MIGHER SIGHTLY: Belongs to the Bowman-Birk serine protease inhibitor
                                                                                                                                                     Pubmed=14703175;
Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C.,
Hild M., Beckmann B., Haas S., Koch B., Sauer F., Hoheisel J., Paro R.;
Pellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J., Paro R.;
An integrated gene annotation and transcriptional profiling approach
towards the full gene content of the Drosophila genome.";
Genome Biol. SIR3.R3(2003).
I- MISCELLANBOUGS: The sequence shown here is derived from an
EMBL/GenBank/DDBJ third party annotation (TPA) entry.
EMBL/SHO03929; DAADSG77.1;
InterPro; IPRO01450; 4Fe45 Ferredoxin.
PROSITE; PS00198; 4Fe45 Ferredoxin.
SEQUENCE S9 AA; 6339 MW; 7BDZC0BSC0F84905 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82249808; PubMed-6125033;
Zhang Y., Luo S., Tan F., Qi Z., Xu L., Zhang A.;
"Complete amino acid sequence of mung bean trypsin inhibitor.";
Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 25:268-277(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-PEB-1995 (Rel. 31, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Bowman-Birk type trypsin inhibitor.
Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae; Vigna.
    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pshydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 2; Length 59;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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Pfam; PF00228; Bowman-Birk_leg; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%;
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PDB, 1DF9, X-ray; C=1-72.
PDB, 1G91, X-ray; I=10-31.
PDB, 1SBW; X-ray; I=8-42.
PDB, 1SWF; X-ray; I=10-31.
InterPro; IPR000877; Prot_ii
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Best Local Similarity 53.3%
....hes 8; Conservative
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                                                                                                                                       SEQUENCE FROM N.A.
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P01062;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE=Liver;
Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
Zhang Y., Liu M., He F.;
Zhang Y., Liu M., He F.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF111848; AAF16687.1;
SEQUENCE : 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.4%; Score 51.5; DB 2; Length 190; 47.1%; Pred. No. 30; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1823;
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Last sequence update)
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Last annotation update)
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                              ProDom; PD002153; Pentaxin; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01020; EGF_1; UNKNOWN_5.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50026; EGF_3; 5.
PROSITE; PS50825; HYR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
InterPro; IPR001759; Pentaxin.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR0012035; VWF_A.
Pfam; PF012494; HTR; 2.
Pfam; PF00184; PR01454; Pentaxin; 1.
Pfam; PF00084; Sushi; 8.
Pfam; PF00084; Sushi; 8.
Pfam; PF00085; PSWA; N.
PRINTS; PR00895; PSWAXIN.
                                                                                                                                                                                                                                                                                                           PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50026; EGF_3; 5.
PROSITE; PS50025; LAM G DOMAIN; 1.
PROSITE; PS00118; PA2 HIS; UNKNOWN_1.
PROSITE; PS50923; SUSHI; 8.
PROSITE; PS50934; VWFA; 1.
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O61G37 C1 Created)
05-UUL-2004 (TrEMBLrel. 27, Last seque
05-UUL-2004 (TrEMBLrel. 27, Last annot
HDC07368.
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Best Local Similarity 57.1%;
Matches 8; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
PRO0529.
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Matches 8; Conservative
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1823 AA;
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NON TER
SEQUENCE
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Q9UI23 RESULT 34 09UI23

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RESULT 35
Q61G37
ID Q61G3
AC Q61G3
DT 05-JU
DT 05-JU
DT 05-JU

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Gaps

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PROSITE; PS00249; PDGF_1; 1. PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                SEQUENCE FROM N.A.
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                                             BAC87611
BAC87611;
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Q91ZH6;
                        RESULT 38
BAC87611
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BMBL; AK120797; BAC89711.1; --
BMBL; AK120797; BGF_11.1; --
BMBL; AK120797; BGF_2, UNXOWN 1.
REOSITE; PS01186; BGF_2, UNXOWN 1.
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ProDom; PD002168; Bowman-Birk_leg; 1.
SMART; SM00269; BowB; 1.
PROSITE; PS00281; BOWMAN BIRK; 1.
3D-structure; Direct profein sequencing; Serine protease inhibitor.
SITE 47 48 Reactive bond for trypsin.
SITE 47 48
                                                                                                             By similarity.
By similarity.
By similarity.
Myssing (in 2nd and 3rd isoinhibitor).
M -> D (in 1st isoinhibitor).
D -> K (in 3rd isoinhibitor).
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Q6ZQS2;
O5_JUL_2004 (TYEMBLrel. 27, Last sequence update)
O5_JUL_2004 (TYEMBLrel. 27, Last annotation update)
O5_JUL_2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ45585.
Hypothetical protein FLJ45585.
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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42.9%; Pred. No. 36;
ive 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                    7959 MW; 8359DE1A8E61E4F8 CRC64;
                                                                   By similarity.
By similarity.
By similarity.
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40 CKSCICTRSMPGKCRCLDT 58
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| | : | | : |
| 9 CLCVCLVSVCLCVC 72
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Best Local Similarity 57.9
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                     72 AA;
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Matches
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Q6ZQS2
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Iria R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDMA sequencing project.";
Submitted (JUL-203) to the EMBL/GenBank/DDBJ databases.
ENBL, AK128797; BAC875111, -
SENBL, AK128797; BAC875111, -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-vegfc; Merions (Mongolian jird) (Mongolian gerbil). Meriones unguiculatus (Mondata; Craniata; Vertebrata; Euteleostomi; Makaryota; Metazca; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

44.0%; Score 51; DB 2; Length 201;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
vascular endothelial growth factor C (Fragment).
                                                   02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ4588 [is, clone BRTHA3013882.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AA.
201
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PRODOM; PRO01629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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PRELIMINARY;
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Gaps
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Name=ENSANG50000008031;

Anopheles gambiae str. PEST.

Blkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-! -GAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAAB01008984; EAA14914.1; -.
NON TER 336 336
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                                                                                            Query Match

44.0%; Score 51; DB 2; Length 326;
Best Local Similarity 36.0%; Pred. No. 55;
Matches 9; Conservative 2; Mismatches 4; Indels
Growth factor; Mitogen.
NON TER 1 1 1
SEQÜENCE 326 AA; 36826 MW; D0B2772C77836914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1
336 336
336 AA; 36383 MW; 0C28D220B6E129A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                          246 CQCVCKRICPRNQPLNPGKCICECT 270
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SEQUENCE
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Query Match 44.0%; Score 51; DB 2; Length 336; Best Local Similarity 55.6%; Pred. No. 56; Matches 10; Conservative 1; Mismatches 3; Indels

Search completed: October 26, 2004, 15:39:20 Job time : 131.5 secs

3 CRCICTRGFC---RCICT 17 | | | | | | 162 CGCTC-RGFCDPHRCACS 178

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APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Van, Jun
APPLICANT: Van, Jun
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
TITLE OF INVENTION: And
PRIOR PILING DATE: 1999-487
PRIOR PILING DATE: 1999-65-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
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                                                                                                                                                                              October 26, 2004, 15:20:02 ; Search time 31.5 Seconds (without alignments) 37.896 Million cell updates/sec
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Sequence 9,
Sequence 9,
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-967-808-9
US-10-141-645-1
US-10-141-645-2
US-10-141-645-4
US-10-141-645-5
US-10-141-645-5
US-09-917-340-53
US-10-141-645-9
US-09-917-340-53
US-10-141-645-9
US-09-967-808-22
US-09-967-808-22
US-09-967-808-22
US-09-967-808-22
US-09-967-808-22
US-10-141-645-68
US-10-141-645-67
US-09-967-808-16
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JS-09-604-864-1
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Maximum Match 100%
Listing first 45 summaries
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112
1 GVCRCLCRRGVCRCLCRR 18
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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58 51.8 17 4 US-10-042-872-1 Sequence 1, Appli 55 50.9 180 4 US-09-510-238A-286 Sequence 286, Appli 56 50.0 9 3 US-09-510-238A-286 Sequence 20, Appli 56 50.0 9 4 US-09-967-808-20 Sequence 20, Appli 56 50.0 9 4 US-10-141-645-27 Sequence 27, Appli 56 50.0 140 4 US-10-141-645-65 Sequence 45, Appli 56 50.0 140 4 US-10-141-645-65 Sequence 65, Appli 56 50.0 140 4 US-10-141-645-69 Sequence 67, Appli 57 58 59.1 168 4 US-09-270-767-40304 Sequence 67, Appli 57 58 59.5 48.7 96 4 US-10-141-645-12 Sequence 67, Appli 58 53.5 47.8 350 2 US-08-929-811-4 Sequence 12, Appli 58 53.5 47.8 350 2 US-08-929-811-4 Sequence 2, Appli 58 53.5 47.8 350 3 US-09-042-105-4 Sequence 4, Appli	ALIGNMENTS SULT 1 -09-309-487-1 Sequence 1, Application US/09309487 Sequence 1, Application US/09309487 Septicant No. 6335318 GENERAL INFORMATION: APPLICANT: Tang, Yi-Quan APPLICANT: Tang, Yi-Quan APPLICANT: Tough Yi-Quan APPLICANT: Vuan, Jun APPLICANT: Outlette, Andre J. TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same FILE REFERENCE: P-UC 3095 CURRENT APPLICATION NUMBER: US/09/309,487 CURRENT APPLICATION NUMBER: US/09/309,487 CURRENT FILING DATE: 1999-05-10 NUMBER OF SEQ ID NOS: 31 SSOTURENT PRICE PATENT OR SEQ ID NO 1 LENGTH: 18 TYPE: PRI ORGANISM: Macaca mulatta -09-309-487-1	ry Match 88.4%; Score 99; DB 3; Length 18; t Local Similarity 83.3%; Pred. No. 8.6e-06; ches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0 1 GVCRCLCRRGVCRCLCRR 18
44 666	RESULT 1 US-09-309-487- 5 Sequence 1, Patent No. 6 GENERAL INFO APPLICANT: AP	Match ocal s 1 1 1 7-808

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82.1%; Score 92; DB 4; Length 18; 66.7%; Pred. No. 5.6e-05; Live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert Leinel.
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE BEFERRACE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 2002-06-6
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: Usassigned
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PastsEQ for Windows Version 4.0
LENGTH: 18
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PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 2
LENGTH: 18
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Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
                                                                                                                                                                                                               Sequence 1, Application US/10141645
Patent No. 6713079
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Best Local Similarity 66.7
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-141-645-1
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Patent No. 6325318;
General No. 6325318;
General Information:
General Informa
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APPLICANT: Tang, Yi-Quan
APPLICANT: Tung, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Outliete, Andre J.
TITLE OF INVENTION: Animicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
TITLE OF INVENTION: Sam
                                                                                                                                                                                                                                                                              Gaps
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0
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Pred. No. 8.6e-06;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
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Best Local Similarity 87.5%; Pred. No. 2.5e-05;
Matches 14; Conservative 1; Mismatches 1.
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Sequence 9, Application US/09967808
Setent No. 6514727
BALEAL INFORMATION:
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                     1 GVCRCLCRRGVCRCLCRR 18
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                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
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US-09-309-487-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
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US-09-309-487-9
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APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-OLICIP
CURRENT APPLICATION WUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
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1 GVCRCLCRRGVCRCLC 16

1 GICRCICGRGICRCYCGR 18

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Query Match

78.6%; Score 88; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00016;
Matches 12; Conservative 3; Mismatches 3; Indels
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78.6%; Score 88; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00016;
Matches 12; Conservative 3; Mismatches 3; Indels
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Retrocyclins - Antiviral
CURRENT FILING DATE: 1020-05-06
PRICR PILING DATE: 2002-06-18
PRICR FILING DATE: 2001-04-18
PRICR FILING DATE: 2002-04-18
PRICR FILING DATE: 2002-04-18
PRICR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASTER OF OF Windows Version 4.0
SEQ ID NO 6
LENGTH: 18
                                                                                                                GENERAL NO. 0.120700:
GENERAL NO. 0.120700:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring:
APPLICANT: Alan Waring:
TYLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Ancimicrobial Peptides:
TITLE REPERENCE: UCLA-001CIP;
FILE REPERENCE: UCLA-001CIP;
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/10/141,645
PRIOR APPLICATION NUMBER: US/10/141,645
PRIOR PRILING DATE: 2001-04-18
PRIOR PRILING DATE: 2002-04-18
PRIOR PLING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-141-645-6
; Sequence 6, Application US/10141645
; Patent No. 6713078
            US-10-141-645-5
Sequence 5, Application US/10141645
; Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |||:||:||:||
1 GYCRCICGRGICRCICGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-141-645-5
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.5%; Score 89; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 0.00012; Matches 12; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS-10-141-045-49
; Sequence 4, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alaw Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: 1001-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PILING DATE: 2002-05-06
PRIOR PELICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PELILNG DATE: 2002-04-18
; PRIOR FILING DATE: 2002-04-18
; RECORTIANT OF THE PRIOR PELICATION NUMBER: TASSIGNED
; RECORD OF SEQ ID NOS: 125
; SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 125
US-12-141-045-3

US-12-141-045-3

Patent No. 6713078

GENERAL INFORMATION:

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alan Waring

APPLICANY: Alexander Cole

APPLICANY: Alexander Cole

APPLICANY: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

FILE REPRENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: 60/284,855

PRIOR PILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-04-18

PRIOR FILING DATE: 2002-04-18

PRIOR PILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SEQ ID NO 3

LENGTH: BASES OF Windows Version 4.0

SEQ ID NO 3

LENGTH: DENGTH: 2008-04-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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1 GVCRCLCRRGVCRCLCRR 18

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1 RCICTRGFCRCLCRR 15

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Score 77; DB 4; Length 18; Pred. No. 0.0031; 4; Mismatches 4; Indels
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                                                                                      APPLICANT: Robert Lehrer
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR PILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: 001-04-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR APPLICATION NUMBER: Unassigned
FRIOR FILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR FILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: Unassigned
FRIOR FILING DATE: 2001-04-18
FRIOR APPLICATION NUMBER: Unassigned
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: 60/284,855
PRICR FILING DATE: 2002-05-06
PRICR FILING DATE: 2002-04-18
PRICR FILING DATE: 2002-04-18
PRICR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEGIL 18
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US-10-141-645-8; Sequence 8, Application US/10141645; Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10141645; Patent No. 6713078; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 55.6%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserva
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US-10-141-645-9
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Pred. No. 0.00036;
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                                                                                                                                                                     APPLICANT: KODELL LELL.
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
FRICH FILING DATE: 2001-04-18
FRICH FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 18
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Fatent No. 6656238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
CURRENT PELING NOWBER: US/09/917,340
CURRENT APPLICATION NUMBER: 6/221,632
PRIOR FILING DATE: 2001-07-29
FRIOR FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-01-17
FRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARS: PatentIN Ver: 2.0
SENDING PATE: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Artificial Sequence : FEATURE: ; OTHER INFORMATION: synthetic variant US-10-141-645-7
                                                         Sequence 7, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVCRCLCRRGVCRCLCRR 18
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Best Local Similarity 61.1%;
Matches 11; Conservative
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; ORGANISM: Macaca mulatta
US-09-917-340-53
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US-09-917-340-53
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Pred. No. 0.91;
1; Mismatches 1; Indels
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APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/0284,855
PRIOR APPLICATION NUMBER: US/0284,855
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2002-04-18
PRIOR PLING DATE: 2002-04-18
SEQ ID NO 5EQ ID NOS: 125
SOFTWARE FABSER FOR FOR MINGOWS VERSION 4.0
SEQ ID NO 68
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Mong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRICR PILING DATE: 2001-04-18
PRICR PILING DATE: 2001-04-18
PRICR PILING DATE: 2002-04-18
PRICR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SUSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
INPE: PRICR PILING
TYPE: PRIC
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CCATION: 113
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-141-645-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
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Patent No. 6713078
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT

// ORGANISM: Orangutan
US-10-141-645-68
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US-10-141-645-72
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Sequence 22, Application US/09309487

Patent No. 6335318

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REPERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/309,487

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 92
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Sequence 22, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

APPLICANT: Yuan, Jun

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

CURRENT FILING DATE: 1000-09-26

CURRENT FILING DATE: 1090-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENTING TIME OF SEQ ID NOS: 31

SEQ ID NO 22

LENTING TIME OF SEQ ID NOS: 31

SEQ ID NO 22
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Pred. No. 0.64;
1; Mismatches 2; Indels
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Pred. No. 0.64;
1; Mismatches
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Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
                       55.4%;
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Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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CRGANISM: Macaca mulatta
US-09-967-808-22
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, ORGANISM: Macaca mulatta
US-09-309-487-22
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US-09-309-487-22
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US-09-967-808-22
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RESULT 17

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53.6%;
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Best Local Similarity 83.5
Local 10, Conservative
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Matches 10; Conservative
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; ORGANISM: Macaca mulatta
US-09-309-487-16
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, ORGANISM: Macaca mulatta
US-09-967-808-16
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LENGTH: 76
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Pred. No. 1.2;
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   APPLICANT: Kudet Lucia...
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA.001C1P
CURRENT APPLICATION NUMBER: 06/284,855
PRIOR APPLICATION NUMBER: 06/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
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Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alaxander Cole
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPRENCE: UGLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
FRICA APPLICATION NUMBER: 60/284,855
FRICA FILING DATE: 2001-04-18
FRICA FILING DATE: 2002-04-18
FRICA FILING DATE: 2002-04-18
FRICA FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SECTIVANE: FASTESEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
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68 RCICRRGVCRFL 79
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APPLICANT: Robert Lehrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Orangutan
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Best Local Similarity
Matches 10; Conserv
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ORGANISM: Orangutan
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TITLE OF UNEXTION: Antimaticable and Methods of Using Same in Processing Processing and Methods of Using Same in Processing Processing Same in Processing
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Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
             Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
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ORGANISM: Limulus polyphemus
US-09-604-864-1
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69 RCICRRGVCOLLRR 82
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; Parent No. 63553108;
GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Or INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REPREBRENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT PILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 21
: LENGTH: 92
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Sequence 21, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Y1-Quan

APPLICANT: Tang, Y1-Quan

APPLICANT: Tang, Y1-Quan

APPLICANT: Tang, Y1-Quan

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

CURRENT APPLICATION NUMBER: US/09/967,808

CURRENT PILING DATE: 2001-09-26

PRIOR PLLING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 21

LENGTH: 22
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Pred. No. 1.1;
1; Mismatches 3; Indels
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Pred. No. 0.94;
1; Mismatches
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 76
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Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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; ORGANISM: Macaca mulatta
JS-09-967-808-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-21
                                                                               TYPE: PRT
ORGANISM: Macaca mulatta
                                                                                                                                          ; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-141-645-17
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US-09-967-808-21
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US-09-309-487-21
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| Seet | March | Sief | Score 60 | DB 44 | Length $27 |
| Beet | Matches | Sief | Score 60 | DB 44 | Length $27 |
| Matches | Siconservative | 1, Mismatches | Si Indels | O; Gaps | O; |
| Matches | Siconservative | 1, Mismatches | Si Indels | O; Gaps | O; |
| Matches | Siconservative | 1, Mismatches | Si Indels | O; Gaps | O; |
| Matches | Siconservative | Sico
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Sequence 20, Application US/09309487

Sequence 20, Application US/09309487

Patent No. 6335318

GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Vian, Jun
APPLICANT: Vian, Jun
APPLICANT: Oxellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Annimicrobial Theta Defensins and Methods of Using TITLE OF INVENTION: Same
FILE REFERENCE: P-UC 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 56; DB 3; Le
red. No. 3.8e+05;
Mismatches 0;
APPLICATION NUMBER: WO PCT/US 96/15774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.9%; Score 57; DB 4; Best Local Similarity 50.0%; Pred. No. 4.2; Matches 8; Conservative 0; Mismatches 8
                                                                         ATTORIAL DATE: 03-01-13-3
ATTORIAL SENENT: DENNIS A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 2910/1
TELECOMMUNICATION INFORMATION:
TELEPHOR: 314-694-5095
INFORMATION FOR SEQ ID NO: 286:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                    FILING DATE: 06-OCT-1996
APPLICATION NUMBER: US 60/004,834
FILING DATE: 05-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 286: US-09-510-238A-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; sc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Macaca mulatta
US-09-309-487-20
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Best Local Similarity
Thes 9; Conserva
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US-09-967-808-20
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MCWHERTER, CHARLES A
STATER, NICHOLAS R
SUWTERS, NEENA L
BAUER, S C
LEE, STEPHEN C
TITLE OF INVENTION: MULTI-FUNCTIONAL HEMATOPOIETIC RECEPTOR
AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                  Sequence 1, Application US/10042872

Patent No. 6747007

GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: THE ADDITION:
TITLE OF INVENTION: USE THEREOF
FILE REPREBROKE: USC170-1
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT APLICATION NUMBER: US 09/604,864
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
LENGTHARE: EastSEQ for Windows Version 4.0

SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 4; Length 17;
Pred. No. 0.47;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNIS A. BENNETT, G.D. SEARLE & CO.,
CORPORATE PATENT DEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 286, Application US/09510238A Patent No. 6730303 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FENG, YIOING
BAUM, CHARLES M
CAPARON, MAIRE H
ZURFLUH, LINDA L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. BOX 5110
  CRCLCRRGVCRCLCRR 18
                                         2 CFAVCRRGRCRYKCRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
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2 CFAVCRRGRCRYKCRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Limulus polyphemus US-10-042-872-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: CHICAGO
STATE: ILLINOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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US-09-510-238A-286
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APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alaxander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antinicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION WUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SUSTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 RCLCRRGVCRCLCR 17
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Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
US-10-141-645-121
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US-10-141-645-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: generated by replacement of variants in consensus; OTHER INFORMATION: sequence US-10-141-645-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                              50.0%; Score 56; DB 4; Length 9; 100.0%; Pred. No. 3.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10141645

Sequence 27, Application US/10141645

GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral
APPLICANT: Decea Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
APPLICANTION Refrection of Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: USS-06
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTHARE: FREESEQ for Windows Version 4.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-141-645-45
Sequence 45, Application US/10141645
Patent Robert Lehrer
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
FILE REFERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
       CURRENT APPLICATION NUMBER: US/09/967,808
                              CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                   Query Match 50.0
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-20
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OTHER INFORMATION: generated by replacement of variants in consensus OTHER INFORMATION: sequence
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Sequence 32502, Application US/09252991A
Patent No. 6551795
GERREAL INFORMATION:
APPLICANT:
Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION WIGHER:
TITLE OF INVENTION:
APPLICATION NUMBER:
US/09/252,991A
PRIOR PELICATION NUMBER:
US/00/074,788
PRIOR PELICATION NUMBER:
US 60/074,788
PRIOR PILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-07-27
NUMBER OF SEQ ID NOS:
33142
SEQ ID NO 32502
LENGTH:
168
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Sequence 40304, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICANTION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 49304

LENGTH: 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 4; Length 168; Pred. No. 6.8;
                                                                                                                                                                                                                                                                DB 4; Length 141;
                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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47.4%; Pred. No. 4.9;
live 3; Mismatches 4;
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.3%; Pred. No. 4.5,
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 125
LENGTH: 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CRCLCRR---GVCRCLCRR 18 | | | | | | | | |
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Best Local Similarity 47.4%;
Matches 9; Conservative
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69 RCICGRGICRLLRR 82
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Best Local Similarity 66.7°
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                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-141-645-125
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                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 4; Length 140;
Pred. No. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-17-141-042-05

| Sequence 69, Application US/10141645
| Patent No. 6713078
| GENERAL INFORMATION:
| APPLICANT: Robert Lehrer
| APPLICANT: Alam Waring
| APPLICANT: Alaxander Cole
| APPLICANT: Alexander Cole
| APPLICANT: Teresa Hong
| TITLE OF INVENTION: Retrocyclins - Antiviral and
| TITLE OF INVENTION: Antimicrobial Peptides
| PRIOR FILING DATE: 2002-04-18
| PRIOR FILING DATE: 2002-04-18
| NUMBER OF SEQ ID NOS: 125
| SOFTWARE: FASTSEQ for Windows Version 4.0
| TITLE OF INVENTION: ANTIMICROBIAL PERIOR FILING DATE: ANTIMICROBIAL PERIOR 
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Patent No. 6713078

GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR PILLNG DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PLILNG DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILLNG DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
US-10-141-645-65
                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                             50.0%;
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Gorilla
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Pb 16 CGCVCQRRCAGVCACECSK 34

RESULT 40
US-09-270-767-55520
Sequence 55520, Application US/09270767
Sequence 55520, Application US/09270767
Sequence 55520, Application US/09270767
SEQUENCE SEGUENCE Elle Reference 1326-094
STILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference 1326-094
STILE OF INVENTION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 55520
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1,

3; Gaps

Query Match
Best Local Similarity 47.4%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 4; Indels

Search completed: October 26, 2004, 15:41:19 Job time : 32.5 secs

3 CRCLCRR---GVCRCLCRR 18 | | : | : | | | | | : 16 CGCVCQRRCAGVCACECSK 34

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Copyright (c) 1993 - 2004 Compugen Ltd.
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283416 seqs, 96216763 residues US-10-009-317A-33 112 1 GVCRCLCRRGVCRCLCRR 18 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	defensin-	theta defensin 1b	hypothetical prote		원	hypothetical prote	Н		_	-1	probable membrane	probable integral	G protein-coupled	AcOrf-70 protein -	hypothetical prote	epidermal growth f	ption	Balbiani ring 3 pr	genome polyprotein	otogelin - mouse	Q300 protein - mou	sterol isc	nel protein - chic	neurotoxin Tx2 - s	pulmonary surfacta	fibronectin recept	hypothetical prote	chloramphenicol re	probable diogenase
SOLVENING	ΙD	C59089	B59089	1565	T24272	869207	T15617	T18975	A59089	T48125	B45878	\$50807	E71602	JC5042	G72858	B70554	EGMSMG	A41116	808167	GNNY21	T42214	I48725	T46871	JP0076	S29214	LNPG1	C37057	D72481	A25854	H90942
	DB													7														7		N
	Length	18	9/	188	164	419	1131	152	16	85	582	131	248	476	290	303	1217	265	1700	2206	2910	77	256	835	53	79	94	128	302	321
dю	Query Match	71.4	53.6	51.8	50.9	47.8	46.9	46.4	45.5	45.5	45.1	44.6	44.2	43.8	42.9	42.9	42.9	42.4	42.0	42.0	42.0	41.5	41.5	41.5	41.1	41.1	41.1	41.1	41.1	41.1
	Score	80	9	28	57	53.5	52.5	52	51	51	50.5	. 20	49.5	49	48	48	48	47.5	47	47	47	46.5	46.5	46.5	46	46	46	46	4.6	4.5
	Result No.		7	M	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

probable dioxygena	probable diogenase	cobyric acid synth	epidermal growth f	restrictin precurs	proteinase inhibit	Bowman-Birk protei	proteinase inhibit	hypothetical prote	hypothetical prote	probable dioxygena	probable cobQ prot	protein F12K21.20	fibronectin recept	hypothetical prote	hypothetical prote
C64941	D85791	C82426	EGRT	JH0675	807405	JC2225	TISYC2	T28784	S02186	AE0304	C70940	H86468	B27079	T15840	\$26689
N	0	N	н	н	N	N	Н	~	~	~	0	N	0	0	0
321	321	484	1133	1353	83	94	103	532	95	321	494	602	798	2946	118
	41.1	41.1	41.1	41.1	40.6	40.6	40.6	40.6	40.2	40.2	40.2	40.2	40.2	40.2	39.7
	46 41.1	46 41.1	46 41.1	46 41.1	45.5 40.6	45.5 40.6	45.5 40.6	45.5 40.6	45 40.2	45 40.2	45 40.2	45 40.2	45 40.2	45 40.2	44.5 39.7

ALIGNMENTS

RESULT 1 C59089 theta defensin-1 - rhesus macaque	N.)Alternate names: xiv.1 C;Species: Macaca mulatta (rhesus macaque) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999	C. Accession: C. Sydes R. Trang, Y. Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Cuellette, A.J.; T. Trang, N.C., Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Cuellette, A.J.;	Science 286, 436-504, 1359 A; Fitle: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A; Reference number: A59089; MUID:99453140; PMID:10521339 A; Accession: C59089	A;Status: preliminary A;Molecule type: protein	AjNote: this sequence is cyclically permuted by -6 residues from the sequence presented i C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089. C;Revwords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing	F;1-9/Region: theta defensin la-derived F;10-18/Region: theta defensin lb-derived F;11-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental F;2-11,4-9,13-18/Disulfide bonds: #status experimental	#scarus ex	Query Match 71.4%; Score 80; DB 2; Length 18; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Oy 4 RCLCRGVCLCRR 18	Db 1. RCICTRGFCRCLCRR 15	BESULT 2 B59089 Holder defensin 1b precursor - rhesus macaque C;Species: Macaca mulatta (rhesus macaque) C;Species: Macaca mulatta (rhesus macaque) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: B59089 C;Ausn, J.; Vuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.; Science 286, 498-502, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Reference number: A59089; MUID:99453140; PMID:10521339 A;Status: preliminary
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A.Cross-references: UNIPROT:PB2271; GB.AF191101; NID:g6137229; PIDN:AAF04390.1; PID:g6137 C;Comment: For the complete mature sequence, see PIR:C59089. C;Superfamily: mammalian defension C;Superfamily: mammalian defension: C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing F;1-20/Domain: signal sequence #status predicted <SIG>

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vascular endothelial growth factor C precursor - human Cippedes: FLT4 ligand DHM Cippedes: Homo sapiens (man) Pspecies: Homo sapiens (man) Cippedes: Homo sapiens (man) Cippedes: J7-Apr-1996 #eequence revision 01-Nov-1996 #text_change 09-Jul-2004 C;Accession: S69207; S61795; $71443; S69208; G02659 R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, B.; Saksela, C R;FBDO J. 15, 1751, 1996 A;Ftle: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for A;Reference number: S69207; MUID:96203094; PMID:8612600 A;Accession: S69207 A;Accession: S69207 A;Accession: Multipspe: Manual A;Molecule type: MANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1.419 <-000>
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e221(
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e221(
A; Cross-references: UNIPROT: P49767; EMBL: X94216; NID: 91177488; PIDN: CAA63907.1; PID: e221(
A; Note: this is a revision to the sequence from reference S61795
A; Note: this is a revision to the sequence from reference S61795
BMBO J: 15, 290-298, 1996
A; Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEA; A; Reference number: S61795; MUID: 96178224; PMID: 8617204
A; Reference number: S61795
A; Molecule type: many
A; Molecule type: many
A; Molecule type: many
A; Molecule type: many
A; Note: this sequence has been revised in reference S69207
A; Accession: S71443
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A;Residues: 'X',104-120 «JOUZ»
R;Lee, J; Gray, A.; Yuan, J; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the BMBL Data Library, December 1995 .
A;Description: Vascular endothelial growth factor related protein (VRF): A ligand and spe
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F):1-12/Domain: signal sequence #status predicted <SIG>
F):13-102/Domain: propeptide #status predicted <PRO>
F):103-419/Product: vascular endothelial growth factor C #status experimental
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15617
R;Bentley, D.
submitted to the EMBL Data Library, October 1995
A;Bescription: The sequence of C. elegans cosmid C25F6.
A;Reference number: Z18377
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Pred. No. 14;
6; Mismatches
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submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.7%;
Matches 8; Conservative
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A;Accession: G02659
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A; Residues: 1-419 <MOR>
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A/Reference number: 219867

A/Reference number: 219867

A/Accession: T24272

A/Accession: T24272

A/Accession: T24272

A/Accession: T24272

A/Accession: DNA

A/Accession: Lafe (WIL)

A/
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Submitted to the EMBL Data Library, May 1996
A; Description: The sequence of C. elegans cosmid C27A2.
A; Reference number: Z18382
A; Accession: T1551
A; Accession: T1551
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuas: 1-188 < NHA>A; Residuas: 1-188 < NHA>A; Residuas: 1-188 < NHA>A; Residuas: 1-188 < NHA>A; Residuas: 1-180 < Residuas: 1-180
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C:Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
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                           F;21-64/Domain: amino-terminal propeptide #status predicted <PRO> F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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                                                                                                                                                                   Score 60; DB 2; Length 76;
Pred. No. 0.81;
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Pred. No. 2.4;
0; Mismatches
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Pred. No. 2.9;
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                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
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A,Map position: 2
A,Introns: 19/3; 91/2
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A;Introns: 20/3; 90/2
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A, Map position: 2
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65 RCICTRGFCRLL 76

2; Indels

Ouery Match
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches

2 VCRCLCRRGVCRCLCRR 18

hypothetical protein C06A1.6 - Caenorhabditis elegans

Rimcharray, A. submitted to the EMBL Data Library, June 1995
A;Reference number: Z19054
A;Accession: T18975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aldelet type: DNA

A; Experimental source: clone C06Al

A; Gene: CESP: C06A1.6

Map position: 2

A; Molecule type: DNA

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Probable membrane protein YJL064w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein HRC131; hypothetical protein J1120
C,Species: Saccharomyces cerevisiae
C,Species: Saccharomyces cerevisiae
C,Species: Sacharomyces cerevisiae
C,Species: Sacharomyces cerevisiae
R,Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A,Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A,Reference number: S50798; MUID:95282514; PMID:7762302
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R;Sarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M.
R;Sarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M.
R;Munogenetics 30, 34-41, 1989
A;Title: A mouse chromosome 17 gene encodes a testes-specific transcript with unusual procaptions and an imper: A45878; MUID:89307395; PMID:2568335
A;Accession: B45878
                                                                                                                                                                                                                                    R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
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A, Residues: 1-582 SAR>
A, Cross-references: UNIPROT: Q62295; GB: M28821
A, Note: this sequence has been corrected in Immunogenetics 31, 283-284 (1990) C, Superfamily: mouse hypothetical protein 2
                                                                                                                          hypothetical protein F16M2.210 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-85 «RIE»
A;Cross-references: UNIPROT:Q9M1V4; EMBL;AL138648
A;Experimental source: cultivar Columbia; BAC clone F16M2
C;Genetics:
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Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 2; Mismatches
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Best Local Similarity
Matches 12; Conserv
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A, Introns: 20/1
A, Note: F16M2.210
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C;Superfamily: mammalian defensin
C;Superfamily: mammalian defensin
C;Superfamily: mammalian defensin
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: signal sequence #status predicted <SIG>F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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A;Cross-references: UNIPROT:Q9XVX3; EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:Cd
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: A59089
R;Tang, Y;Q; Yuan, J;Osapay, G;Osapay, K; Tran, D; Miller, C.J;Ouellette, A.J.;
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation C
A;Reference number: A59089
A;Accession: A59089
A;Accession: A59089
A;Accession: C;Carana
A;Residues: 1-76 <TAN>
A;Residues: 1-1131 <BEN>
A;Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F9
                                                           C;Genetics:
A;Gene: CESP:C25F6.2
A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1;
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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18975
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Length 152;

5;

Score 52; DB 2 Pred. No. 11; 0; Mismatches

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Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative (

67 GGGGCCCRPRCCCCCR 83

1 GVCRCLCRRGVCRCLCR 17

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8; Indels

Query Match
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 8; Conservative 1; Mismatches 3; Indels

4 RCLCRRGVCRCL 15

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Cikeywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein; E;34-57/Domain: transmembrane #status predicted <TM1>
F;71-93/Domain: transmembrane #status predicted <TM2>
F;10-129/Domain: transmembrane #status predicted <TM3>
F;107-129/Domain: transmembrane #status predicted <TM3>
F;108-129/Domain: transmembrane #status predicted <TM4>
F;148-172/Domain: transmembrane #status predicted <TM4>
F;199-222/Domain: transmembrane #status predicted <TM6>
F;377-398/Domain: transmembrane #status predicted <TM6>
F;377-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;407-430/Domain: transmembrane #status predicted <TM7
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 09-Ju1-2004
C;Accession: B70554
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
            A;Residues: 1-476 <-...
A;Residues: 1-476 <-...
A;Cross-references: UNIPROT:093126; DDBJ:D78363; NID:g1514430; PIDN:BAA11375.1; PID:g1514
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1.303 <COL>
A,Cross-references: UNIPROT:006545, GB:Z95584, GB:AL123456, NID:g3261774, PIDN:CAB09033.3
A,Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:13,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:230,240,250,260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F:355/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-290 <AXR>
A;Cross-references: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g559139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: G72858
F;Ayres, M.D; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACOFF-70 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 49;
3; Mismatches 6
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Pred. No. 47;
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442 LCKCVCRRGAMERRFRR 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 43.8%;
Similarity 47.1%;
8; Conservative
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ilarity 52.9%;
Conservative
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nes 9; Conserv
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Best Local Similarity
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                        A,Cross-references: UNIPROT:P47038; EMBL:Z34288; NID:9498992; PIDN:CAA84058.1; PID:94990
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
A;Reference number: S47117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum) (S.Species: Dlasmodium falciparum C.Species: Dlasmodium falciparum C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C;Accession: E71602 F. Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: i-248 <GAR>
A.Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:g3845316; PIDN:AAC7197
A.Experimental source: clone 3D7
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Rjisoal, A.; Kawahara, H.; Okazaki, Y.; Shizuri, Y.
Gene 175, 95-100
Ajfithe: Molecular cloning of a new member of the putative G protein-coupled receptor (A; Accession: JCS042; MUID:97074655; PMID:8917082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71602
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C;Species: Balanus amphitrite (barnacle)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:Z49340; NID:g1008212; PID:g1008214; MIPS:YJL064w
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Superfamily: Saccharomyces probable membrane protein YJL064w; Keywords: transmembrane protein
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A; Residues: 1-131 - VAMA-
A; Residues: 1-131 - VAMA-
A; Cross-references: EMBL: 234288; NID: 949892; PID: 9499002
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
B; Vandenbol, Sefesis Sequence Database, September 1995
A; Reference number: $56835
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17;
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Pred. No. 28;
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Pred. No.
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: SGD:S0003600
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Residues: 1-131 <POH>
A;Residues: 1-131 <VAN>
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                                                                                                                                                                                                                                                                        Accession: S47126
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Lranscription factor AWT1, metal-inducible - yeast (Candida glabrata)
C;Species: Candida glabrata
C;Species: Candida glabrata
C;Species: Candida glabrata
C;Species: Char-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41116
R;Zhou, P.; Thiele, D.J.
Proc. Natl. Acad. Sci. US.A. 88, 6112-6116, 1991
A;Title: Isolation of a metal-activated transcription factor gene from Candida glabrata b
A;Reference number: A41116; MUID:91296771; PMID:2068090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalbian ring 3 protein - midge (Chironomus tentans)
C;Species: Chironomus tentans
C;Accession: S08167
R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J; Mol. Biol. 211, 331-349, 1990
A;Reference number: S08167; MUD:90172404; PMID:1689777
A;Accession: S08167
A;Status: not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039-1063/Domain: transmembrane #status predicted <TMM>
1064-1217/Domain: intracellular #status predicted <INT>
1347-360,366-377,373-386,388-401,407-418,414-427,429-442,445-457,453-467,469-482,751-76
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A,Residues: 1-265 <ZHO>
A,Cross-references: UNIPROT:P41772; GB:M69146; NID:g173319; PIDN:AAA35271.1; PID:g173320
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A; Cross-references: UNIPROT: Q03376; GB: X52263; NID: 97057; PIDN: CAA36506.1; PID: 97058
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F;573-615/Domain: LDL receptor YWTD-containing repeat homology <YW015-515/Stomain: LDL receptor YWTD-containing repeat homology <YW018-515/Stomain: LDL receptor YWTD-containing repeat homology <YW018-515/Stomain: LDL receptor YWTD-containing repeat homology <YW105-77-17-186/Domain: LDL receptor YWTD-containing repeat homology <YW10-78/101-743/Domain: LDL receptor YWTD-containing repeat homology <YW10-78/101-743/Domain: EGF homology <EG5-7-1881-917/Domain: EGF homology <EG5-7-1929/Stomain: EGF homology <EG8-7-1019/Domain: EGF-7-1019/Domain: EGF-7-1019/D
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66.7%; Pred. No. 50;
tive 0; Mismatches 4; Indels
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22.6%;
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Best Local Similarity 66.7%
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Best Local Similarity
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A;Accession: A93304
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-789, V. 791-1047, S',1049-1168 <GRA>
A;Cross-references: GB:J00380
A;Cross-references: GB:J00380
A;Note: the sequence shown by these authors differs from residues 1134-1168 due to an in uence of Scott et al.)
B;Savage Jr., C.R.; Inagami, T.; Cohen, S.
J. Biol. Chem. 247, 7612-7621, 1972
A;Title: The primary structure of epidermal growth factor.
A;Reference number: A92118; MUID:73048516; PMID:4636327
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C. Comment: EGF is released in the pancreas, small intestine, mammary gland, and (in some C. Comment: The EGF precursor is found in kidney as a receptor-like membrane-bound protein C. Comment: The active growth factor from this submaxillary gland protein stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whatermal growth factor precursor - mouse bydermal growth factor precursor - mouse bydermal growth factor precursor C; Matternate names: urogastrone precursor C; Species: Mus musculus (house mouse) C; Date: 30-Nov-1980 #sequence_revision 11-Aug-1983 #text_change 09-Jul-2004 C; Date: 30-Nov-1980 #sequence_revision 11-Aug-1983 #Text_change 09-Jul-2004 R; Scott, J; Urdea, M.; Quiroga, M.; Sanchez-Pescador, R.; Fong, N.; Selby, M.; Rutter, Science 21, 236-240, 1983 #Title: Structure of a mouse submaxillary messenger RNA encoding epidermal growth factor A; Reference number: A94272; MUID:83223630; PMID:6602382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA

A Kesidues: 1-127 <SCO>

A Cross-references: UNIPROT:P01132, GB:J00380, NID:g192993, PIDN:AAA37539.1, PID:g309210

R;Gray, A.; Dull, T.; Ullrich, A.

R;Gray, A.; Dull, T.; Ullrich, A.

R;Gray, A.; Dull, T.; Ullrich, A.

A;Title: Nucleotide sequence of epidermal growth factor cDNA predicts a 128,000-molecula

A;Reference number: A93304; MUID:83219309; PMID:6304537
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A; Residues: 977-1029 < SAV >
A; Residues: 977-1029 < SAV >
A; Residues: 977-1029 < SAV >
A; Molecules: 977-1029 < SAV >
A; Molecules: 977-1029 < SAV >
A; Molecules: 1024-1029 < SAV >
J. B; Ol. Chem. 248, 7669-7672, 1973
J. B; Ol. Chem. 248, 7669-7672, 1973
A; Title: Epidermal growth factor. Location of disulfide bonds.
A; Reference number: A92144; MUID:7405498; PMID:4750422
A; Contents: amoutation, disulfide bonds
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                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                        Length 303;
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Pred. No. 48;
0; Mismatches
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ilarity 60.0%;
Conservative
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Best Local Similarity
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                                 C,Genetics:
A,Gene: Rv1145
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Matches

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O300 protein - mouse
C;Species: Mus wusculus (house mouse)
C;Species: Mus wusculus (house mouse)
C;Accession: 148725
Bsequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148725
Bsequence_revision 03.7 Knippersr_R.
J. Virol. 65, 3259-3267, 1991
A;Title: The Q300 gene: a novel transcription unit induced in simian virus 40-infected ar A;Reference number: 148725, MUD:91237845; PMID:1851876
A;Reference number: 148725
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-77 <RES.
A;Residues: 1-77 <RES.
A;Cross-references: UNIPROT:Q02722; EMBL:X52164; NID:953860; PIDN:CAA36417.1; PID:953861
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A.Alternate names: delta 8-vdelta 7 sterol isomerase
C:Species: Neurospora crassa
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
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A/Gene: eron:
A/Map position: V
A/Introns: 145/1
C/Keywords: intramolecular oxidoreductase; isomerase; sterol biosynthesis
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 64;
0; Mismatches
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Best Local Similarity 53.3%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches
724 CRRDACRCGQPCLCATLAHYARLCRR 749
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R;Gilbert, 'J; Orbach, M.J.
submitted to the EMBL Data Library, May 1996
A; Reference number: 224117
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A;Cross-references: UNIPROT:Q92254; EMBL
A;Experimental source: strain OR23-74-1A
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Best Local Similarity 66.7%;
Matches 8; Conservative
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"Residues: 1-2206 4HUG>
"Residues: 1-2206 4HUG>
"Residues: 1-2206 4HUG>
"Residues: 1-2206 4HUG>
"Processor of the service of t
                                                                                                                                                                                                                                                                                                                                 genome polyprotein - coxsackievirus A21 (strain Coe)
N.Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core propolymerase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1.2910 <COH>
(Cross-references: UNIEROT:055225; EMBL:U96411; NID:g2760883; PID:g2760884; PIDN:AAB965; Experimental source: strain BALB/c
(Accest component of all the acellular membranes of the inner ear
(Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cohen-Salmon, M.; Bl-Amraoui, A.; Leibovici, M.; Petit, C. roc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997; Steference number: 222079; MulD:98070772; PMID:9405633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: A33373 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: A33373 #s. July North, C.; Minor, P.D.; Stanway, G. R,Hughes, P.J.; North, C.; Minor, P.D.; Stanway, G. A;Title: The complete nucleotide sequence of coxsackievirus A21. A;Reference number: A33373; MUID:90063544; PMID:2584950
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
    Gaps
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F,1029-1125/Product: Core protein 28 #status predicted <PB2>
F,1126-1453/Product: Core protein 28 #status predicted <PB2>
F,1454-1540/Product: protein 3A #status predicted <PA3>
F,1541-1562/Product: genome-linked protein VPg #status predicted <PB3>
F,1561-1745/Product: genome-linked protein VPg #status predicted <PB3>
F,1561-1746-2206(Froduct: RNA-directed RNA polymerase #status predicted <PD3
F,1543/Binding site: phosphory1-RNA (Tyr) (covalent) #status predicted
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    16;
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Best Local Similarity 52.9%; Pred. No. 2.2e+02;
Matches 9; Conservative 1; Mismatches 7; Indels
    Indels
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    'n
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                                                                                                                                                          1245 CRCVCPROMEKPADNCKTRWWNDEMCQCVCK 1275
    Mismatches
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    9
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7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: coxsackievirus A21
                                                                                 3 CRCLCRRG----
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C.Species: Cavia porcellus (guinea pig)
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 16-Aug-2004
C.Date: 15-Feb-1991 #sequence of the complete aniho acid sequence of a novel integrin beta subunit (beta6) identified A; Reference number: A37057; MUID:901307659; PMID:2365683
A.Accession: C37057
A; Reference preliminary; not compared with conceptual translation
A; Residues: 1-94 GSHE>
A; Residues: 1-94 GSHE>
A; Cross-references: GB:J0552
A; Cross-references: GB:J0552
C; Superfamily: Integrin beta chain; laminin-type EGF-like homology
C; Keywords: cell adhesion; duplication; heterodimer; membrane protein
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-128 «KAW>
A,Cross-references: UNIPROT:Q9Y8Z2; DDBJ:AP000064; NID:g5105945; PIDN:BAA81508.1; PiD:dl(
A,Experimental source: strain Kl
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72481
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaht
By H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrt
A;Reference number: A72450; MUID:99310339; PMID:10382966
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Best Local Similarity 47.6%; Pred. No. 47;
Matches 10; Conservative 2; Mismatches 5; Indels
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Pred. No. 39;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       fibronectin receptor beta chain - guinea pig (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVCR----CLCRRGVCRCLCR 17
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                              |:|:|| | : ||
44 GICQCLAERYIVICL 58
                                 1 GVCRCLCRRGVCRCL 15
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A; Gene: APE2492
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NyAlternate names: low molecular mass surfactant protein type 1
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: 3L-bec-1991 #sequence_revision 31-bec-1991 #text_change 09-Jul-2004
Ciscession: 500363
KiCurstedt, T.; Johansson, J.; Barros-Soederling, J.; Robertson, B.; Nilsson, G.; Westbe Bur. J. Blochem. 172, 521-525, 1988
Aprite: Low-molecular-mass surfactant protein type 1. The primary structure of a hydrop Apreference number: 800363; MUID:88166729; PMID:3350011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotoxin Tx2 - spider (Phoneutria nigriventer)
C;Species: Phoneutria nigriventer
C;Species: Phoneutria nigriventer
C;Cpate: 19-Mar-1997
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
R;EBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the vench A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Granner C. S. Species C. Species 
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A; Molecule type: UNIX-
B; Mesidues: 1-79 CUNX-
A; Cross-references: UNIX-
B; C: Comment: Pulmonary surfactant protein is a phospholipid-protein complex, which reduces
C; Comment: Pulmonary surfactant protein B; saposin repeat homology
C; Superfamily: pulmonary surfactant protein B; saposin repeat homology
C; Keywords: alveolar proteinosis; gaseous exchange; lipoprotein; lung; pulmonary surfact
P;1-79/Domain: saposin repeat homology <SAP>
                      R. Wocksthashin, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K. submitted to JIPLD, January 1995
submitted to JIPLD, January 1995
submitted to JIPLD, January 1995
submitted to JIPLD, January 1995
A.Reference number: JP0076
A.References: DBJ:D45365
A.Cross-references: DBJ:D45365
A.Gross-references: DBJ:
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41.5%; Score 46.5; DB 2; Length 835;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels
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41.1%; Score 46; DB 1; Length 79;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 5; Indels
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A; Experimental source: 9-day embryo
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A;Molecule type: protein
A;Residues: 1-53 <COR>
C;Superfamily: curtatoxin
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epidermal growth factor precursor - rat
N;Alternate names: urogastrone precursor
C;Species: Rattus norvegicus (Norway rat)
                                                                                 268 CLCREGVC 275
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                               CLCRRGVC 12
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A,Molecule type: DNA
A,Residues: 1-321 <STO>
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A;Accession: A25854
A;Molecule type: DNA
A;Residues: 1-302 -DOR>
A;Cross-references: UNIPROT:P12056; GB:M22614; NID:g151802; PIDN:AAA26079.1; PID:g151803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Aolecule type: DNA
A;Residues: 1-31 <HAY>
A;Cross-references: UNIPROT:Q8XDR8; GB:BA000007; PIDN:BAB35935.1; PID:g13361979; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cipaces: Escherichia coli
Cidacesion: C64941
Shatuner, F.R.; Plunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Science 277, 1453-1462, 1997
A; Rese, D.G.; Mau, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: H90942

C;Accession: H90942

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

BNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc

A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             robable diogenase beta subunit (imported] - Bscherichia coli (strain 0157:H7, substrain
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EXperimental source: strain K-12, substrain MG1655
Superfamily: Phthalate dioxygenase reductase, cytcohrome-b5 reductase homology; ferred; 11-225/Domain: cytcohrome-b5 reductase homology cCBR>;254-309/Domain: ferredoxin [2Re-25] homology cFR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: ECs2512
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
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Pred. No. 82;
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Pred. No. 85;
0; Mismatches
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                                                                                                        C,Genetics:
A,Gene: cml
A,Gene: plasmid
A,Genee: plasmid
C,Superfamily: bicyclomycin resistance protein
C,Keywords: antibiotic resistance
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Local Similarity 57.1%;
les 8; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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35 CVSRFGHDRCICRR 48
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probable diogenase beta subunit yeax [imported] - Escherichia coli (strain O157:H7, subst C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: D55791
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain 0157:H7, substrain EDL933
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C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredd
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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Pred. No. 85;
0; Mismatches 1; Indels
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A;Map position: 2
C;Superfamily: probable cobyric acid synthase
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative ;
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A, pacesion: P60385
A, Molecule type: protein
A, pacesion: P60385
A, Molecule type: protein is a neural extracellular matrix protein implicated in neural cel
A, Rolecule type: protein is a neural extracellular matrix protein is protein; gel phomology; fibrinogen beta/gamma homology; fibrinogen beta/gamma homology; fibronectin type
C, Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C, Superfamily: restrictin #status predicted < MAT>
F, 130-329 / Domain: EGF homology < EGG>
F, 34-1353 / Product: restrictin #status predicted < MAT>
F, 234-26 / Domain: EGF homology < EGG>
F, 265-29 / Domain: Eibronectin type III repeat homology < FNIS>
F, 324-49 / Domain: fibronectin type III repeat homology < FNIS>
F, 684-76 / Domain: fibronectin type III repeat homology < FNIS>
F, 261-29 / Domain: fibronectin type III repeat homology < FNIS>
F, 261-29 / Domain: fibronectin type III repeat homology < FNIS>
F, 361-34 / Domain: fibronectin type III repeat homology < FNIS>
F, 361-39 / Domain: fibronectin type III repeat homology < FNIS>
F, 361-39 / Domain: fibronectin type III repeat homology < FNIS>
F, 361-39 / Domain: fibronectin type III repeat homology < FNIS>
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F, 361-39 / Domain: fibronectin type III repeat homology < FNIS>
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F, 361-39 / 260 / Domain: fibronectin type III repeat homology < FNIS
F, 372-1286 / FREGEROM (FNIS) / FNIS 
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Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cipate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
Cipacession: JH0675; PS0385; $\overline{\text{S23284}}$ & \overline{\text{S23284}}$ & \overline{\text{S23265288}}$                                                                                                                                                                                                                                                                                                                                                                                                                F;1036-1060/Domain: transmembrane #status predicted <TWM>
F;1061-1133/Domain: intracellular #status predicted <INT>
F;342-355,361-372,368-381,383-396,402-413,409-422,424-437,440-452,448-462,464-477,747-758
-1015/Disulfide bonds: #status predicted
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A,Residues: 1.1533 «US)
A,Cross-references: UNIPROT:Q00546; GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
A,Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
F,656-696/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F,697-739/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F,747-782/Domain: EGF homology <EG5>
F,839-812/Domain: EGF homology <EG7>
F,978-914/Domain: EGF homology <EG7>
F,978-914/Domain: EGF homology <EG8>
F,978-914/Domain: EGF homology <EG8>
F,979-1024/Product: epidermal growth factor #status experimental <MAT>
F,979-1015/Domain: EGF homology <EG8>
F,005-1060/Domain: tansmembrane #status predicted <TMM>
F,1036-1060/Domain: intracellular #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.1%; Score 46; DB 1; Length 1133; Best Local Similarity 37.5%; Pred. No. 1.9e+02; Matches 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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41.1%; Score 46; DB 1;
Best Local Similarity 27.8%; Pred. No. 2.1e+02;
Matches 10; Conservative 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763 GTAQCLCREGEVKAPDGKMCLTRK 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVCRCLCRRGVCR-----CLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CRCLC-
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S07405
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A, Statuers preliminary
A, Molecule type: protein
A, Residues: 974-1021 (NDS)
Biochim. Biophys. Acta 1037, 388-393, 1990
A, Molecule type: protein
A, Reference number: SO8288
A, Molecule type: protein
A, Residues: 974-1034 (NDS)
C, Comment: Egg is released in the pancreas, small intestine, mammary gland, and (in some c, Comment: Egg is released in the pancreas, small intestine, mammary gland, and (in some c, Comment: Egg is released in the pancreas, small intestine protein
C, Superfamily: spidermal growth factor proteinsor; Egg homology, in Di receptor YWTD-condition of C, Superfamily: spidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-103/Pomain: spide is ginal sequence #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 22-1133/Product: epidermal growth factor proprotein, membrane-bound form #status predicted < SIGO F; 23-1135/Promain: EGF promology *SIGO F; 23-1135/Promain: EGF promology *EG3 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Reference number: S05074

A) Accession: S05074

A) Accession: S05074

A) Accession: S05074

A) Residues: W, 966, RWL, 970-1023, NW', 1026-1108, SCAGUSSGPQPWFVVLE', 1126, 'HQ' <SIM>
A) Recadues: W', 966, RWL', 970-1023, NW', 1026-1108, SCAGUSSGPQPWFVVLE', 1126, 'HQ' <SIM>
A) Cross-references: EMBL:X12748

A) Title: Cloning and Sequence analysis of a CDNA for rat epidermal growth factor.

A) Recession: S01974

A) Recession: S01974

A) Molecule type: mRNA

A) Accession: S01974

A) Molecule type: MRNA

A) Molecule type: MRNA

A) References: EWBL:X12748

A) Molecule type: MRNA

A) References: EWBL:X12748

A) Molecule type: MRNA

A) Molecule type: MRNA

A) Molecule type: MRNA

A) Molecule type: MRNA

A) Reference number: A25425; MUID:86081810; PMID:3000762

A) Residues: 974-1021 <SIZ

A) Molecule type: protein

A) Residues: 974-1021 <SIZ

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C;Species: Givenue max (Soybean)
C;Species: Givenue max (Soybean)
C;Bate: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A22636; A01302
R;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
G;Biol. Chem. 259, 9889-9890, 1984
A;Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease inh A;Aceterence number: A92489; MUID:84264652; PMID:6086657
A;Reference number: A92489; MUID:84264652; PMID:6086657
A;Rontents: annotation
A;Note: the sequence has been revised in reference A92540
B;Hammond, R.W.; Poard, D.E.; Larkins, B.A.
J; Biol. Chem. 260, 7806, 1985
A;Reference number: A92440
 Ajaccession: A22636
Ajaccession: A22636
Ajaclecule type: DNA
Ajaclecules: 1-103 «HAM»
Ajacss-references: UNIPROT: P01063; GB:K01967; NID:g169942; PIDN: AAA33952.1; PID:g169943
Rj. Codani, S.; Krenaka, T.
J. Biochem. 82, 1523-1531, 1977
AjTitle: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a soy A; Reference number: A01302; MUID: 78087480; PMID: 599141
 A;Residues: 28-103 <0DA>
C;Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interaction by the protein inhibits trypsin, elastase, and chymotrypsin. The site of interaction shownan-Birk proteinase inhibitor.
C;Superfamily: Bowman-Birk proteinase inhibitor
C;Reywords: duplication; seed; serine proteinase inhibitor
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-103/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental <MAT>
F;28-103/Product: proteinase inhibitor repeat homology <BB1>
F;69-54/Domain: Bowman-Birk inhibitor repeat homology <BB2>
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F;69-54/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted
F;76/Inhibitory site: Ala (elastase) #status predicted
F;76/Inhibitory site: Arg (trypsin) #status experimental
 A;Cross-references: UNIPROT:001972; EMBL:AF003740; PIDN:AAC48138.1; GSPDB:GN00019; CESP:CA;Experimental source: strain Bristol N2; clone C41D11
 Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis elegans
Cispedies: Tagans
Ainaggi, L.
Ai
 <u>ب</u>
 A;Map position: 1
A;Introns: 62/3; 172/1; 403/3; 478/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C41D11.3
 Score 45.5; DB 1; Length 103; Pred. No. 47; 0; Mismatches 3; Indels
 hypothetical protein C41D11.3 - Caenorhabditis elegans
 40.6%;
Local Similarity 60.0%;
les 9; Conservative (
 62 RCACTRSMPGQCRCL 76
 4 RCLCRR---GVCRCL 15
 71 RCACTRSMPGQCRCL 85
 Molecule type: protein; Residues: 28-103 < ODA>
 A;Residues: 1-532 <GAT>
 C;Genetics:
A;Gene: CESP:C41D11.3
 A; Molecule type: DNA
 Accession: A01302
 Query Match
 RESULT 38
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 A.Status: pressment.
A.Status: pressment.
A.Residues: 1-83 «JOU»
A.Residues: 1-83 «JOU»
A.Cross-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g1699
A.Cross-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g1699
A.Cross-references of codons 8-13 and 14-27 are interchanged in the authors' translat R;Baek, J.M.; Kim, S.I.
Submitted to the EMBL Data Library, October 1992
A.Croscribtion: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
 C;Species: Glycine max (soybean)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000
C;Accession: JC2225
R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Biosci, Biotechinol. Biochem. 28, 843-846, 1994
A;Title: Nucleotide sequence homology of CnNAs encoding soybean Bowman-Birk type protein
A;Reference number: JC2224; MUID:94289861; PMID:7764974
 C; Species: Glycine max (soybean)
C; Species: Glycine max (soybean)
C; Date: 02-Dec-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C; Accession: S07405; S29608; S40113
R; Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A; Title: Isolation and sequence of CDNA encoding the soybean protease inhibitors PI IV
A; Reference number: S07405
 A;Molecule type: DNA
A;Residues: 1-83 <GTO>
A;Residues: BBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
A;Crose-references: EMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Keywords: serine proteinase inhibitor
F;22-48/Domain: Bowman-Birk inhibitor repeat homology <BBI>
F;49-74/Domain: Bowman-Birk inhibitor repeat homology <BBI>
 Residues: 1-94 <BAE>
.Comment: This protein regulates endogeneous proteinase during germination, stores sul
 Start codon: GTT

Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology;
Superfamily: Bowman-Birk proteinase inhibitor
11-18/Domain: signal sequence #status predicted <SIG>
11-18/Domain: signal sequence #status predicted <SIG>
119-94/Product: Bowman-Birk proteinase isoinhibitor C-II #status predicted <MAT>
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160-85/Domain: Bowman-Birk inhibitor repeat homology <BBI>
 Cross-references: EMBL:X68705; NID:g18567; PIDN:CAA48656.1; PID:g18568; Giordano, A.; Delledonne, M.; Fogher, C.; Marchetti, S. ubmitted to the EMBL Data Library, December 1993; Degcription: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
 ä
 Gaps
 Bowman-Birk proteinase isoinhibitor C-II precursor (clone pB24) - soybean
 Gaps
 3.
 .,
B
 Length 83;
 Length 94;
 Indels
 Indels
 Query Match
40.6%; Score 45.5; DB 2;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 3;
 DB 2;
proteinase inhibitor (Bowman-Birk) C-II - soybean
 Score 45.5; D
Pred. No. 41;
0; Mismatches
 Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
 4 RCLCRR---GVCRCL 15
 Reference number: S40113
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-83 <BAE>
 Molecule type: mRNA; Residues: 1-94 <BAE>
 A;Status: preliminary
 Status: preliminary
 A; Accession: S07405
 RESULT 36
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 Gaps
 3
Query Match
40.6%; Score 45.5; DB 2; Length 532;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 6; Indels
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Query Match 40.2%; Score 45; DB 2; Length 95; Best Local Similarity 52.6%; Pred. No. 51; Matches 10; Conservative 1; Mismatches 4; Indels

1 GVCRCLCRRGVCRC---LC 16

8 GVCLCVC-FSVCMCVHVLC 25

a

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A,Status: preliminary A,Molecule type: DNA A,Residues: 1-321 <KUR> A,Cross-references: UNIPROT:Q8ZDR4; GB:AL590842; PIDN:CAC91297.1; PID:g15980486; GSPDB:G C, Genetics:

A;Gene: YPO2492 C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred Gaps ; 0 Length 321;

5 CLCRRGVC 12

Search completed: October 26, 2004, 15:40:21 Job time: 25.5 secs

hypothetical protein SP5 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
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C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004
C;Accession: S0186
R;Nishimatsu, S.I.; Murakami, K.; Mitsui, Y.; Ishida, N.
Nucleic Acids Res. 16, 11831-11832, 1988
A;Title: Mouse spleen derived cDNA clones containing per repeat sequence.
A;Reference number: S02186; MulD:89098345; PMID:3267239
A;Accession: S02186
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A;Accession: S02186
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A;Coss-references: UNIPROT:P15974; EMBL:X12806; NID:953649; PIDN:CAB42649.1; PID:948037 298 CGCSCENGVCLPETCQC 314 3 CRCLCRRGVC---RCLC 16

Gaps

probable dioxygenase beta chain YPO2492 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
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C;Date: O2-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 16-Aug-2004
C;Accession: AE0304
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
A;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360

Query Match
40.2%; Score 45; DB 2; Length 321
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels

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1146
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1150
23015
23015
23015
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1134
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Q6ZMP3;
Q6ZMP3
 SEBUTAGE
 g
 Bad18682 homo sapi

P82271 macaca mula

C96912 mus musculu

C6984 mus musculu

C86720 mus musculu

Aah61079 mus musculu

Aah61079 mus musculu

C2048 caenorhabdi

C22048 caenorhabdi

C22048 caenorhabdi

C22048 caenorhabdi

C32048 caenorhabdi

C32049 caenorhabdi

C3491 oryza sativ

C9121 homo herpe

C6799 rattus norv

Aar24072 rattus norv

Aar24072 rattus norv

Aar24072 caenorhabdi

C6752 homo sapien

C77406 anopheles g

C77407 caenorhabdi

C81nd drosophila

C981nd drosophila

C981nd drosophila

C6535 coturnix co

C6535 coturnix co

C6535 homo sapien

C90000 drosophila
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 ; Search time 128.5 Seconds (without alignments) 80.597 Million cell updates/sec
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1825181 segs, 575374646 residues
 SUMMARIES
 062022
BAC87611
BAC87611
QOYWV7
QORIND6
QORIND2
QOST352
QOST352
VEGC HUMAN
QEFF59
AAH63685
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 October 26, 2004, 15:13:56
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 AAR24072
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1 GVCRCLCRRGVCRCLCRR 18
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Gapop 10.0 , Gapext
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length: 2000000000
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 Length
 %
Query
Match
 Title:
Perfect score:
 sed
 Scoring table:
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Run on:
 Result
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TISSUE-TONGUE:

A Tailgami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

A Tailgami A., Fujiwara T., Shibahara T., Ozaki K., Sugiyama T.,

A Makebe H., Ono T., Hishigaki H., Wakamatsu A., Ishii S., Yamamoto J.,

A Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,

A Irie R., Awasi-Irio Y., Sato K., Nishikawa T., Kimura K.,

A Isono Y., Kawai-Irio Y., Sato K., Nishikawa T., Kimura K.,

A Mashita H., Matsuo K., Nakamura Y., Sehine M., Kikuchi H.,

A Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,

Ragiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,

A Masuho Y., Nagai K., Isogai T.;

B Masuho Y., Nagai K., Nagai K., Nagai K., Nagai M., Nagai K., Nagai M., Nagai K., Nagai M., Nagai K., ï
 Q8bcc mus musculu
Q9bcs homo sapien
Q6qcs brachydanio
Q9xvx3 caenorhabdi
Q8irl drosophila
Q8iq18 drosophila
Aan10358 drosophil
Q79c4 anopheles g
Q8bw14 mus mopheles g
Q8bw14 mus musculu
Q8bw16 homo sapien
 086502 mus musculu
der599 mus musculu
Aar8724 mus musculu
Q8bpc0 mus musculu
Q96554 homo sapien
069p2 brachydanio
09xvx3 caenorhabdi
 trypanosoma
mus musculu
mus musculu
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Gaps
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BAD18682;
12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Kinase C, delta type (EC 2.7.1.-).
Homo sapiens (Human).
 3;
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 Indels
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05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16784.
Homo sapiens (Human).
 Query Match
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches
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08C9N2
08C9N2
08BPC0
08BPC0
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06GP2
09SYX3
09SYX3
09SYX3
08IN10358
07PG24
08N962
 177 VCQCLC---VCQCLC 188
 2 VCRCLCRRGVCRCLC 16
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Gaps

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1; Indels

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANLE-2019174; PubMed=11041159;
MEDLINE=2049974; PubMed=11041159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
 the RIKEN Genome Expension Research Group Phase I & II Team; the RIKEN Genome Example of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 SEQUENCE FROM N.A.
STRAIN=CSTBL/6d; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSCRLUM;
"Punctional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
 Score 60; DB 2; Length 76; Pred. No. 1.4;
 THETA DEFENSIN-1, SUBUNIT B. REMOVED IN MATURE FORM.
 F0B754466156071E CRC64;
 STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 PIR; BS9089; BS9089.
GO; GO:0050812; Pickefense response to fungi;
GO; GO:0006805; P:xenobictic metabolism; IEA.
InterPro; IPR002366; Defensin_propep.
Pfam; PF00879; Defensin_propep; I.
Antibiotic; Defensin; Fungicide; Signal.
 168 AA
 1; Mismatches
 PRT;
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
EMBL; AF184156; AAF07923.1; -.
 8189 MW;
 53.6%;
 83.3%;
 Local Similarity 83.3
hes 10, Conservative
 4 RCLCRRGVCRCL 15
 PRELIMINARY;
 65 RCLCRRGVCOLL 76
 64
73
76
 Mus musculus (Mouse).
 SECUENCE FROM N.A.
 76 AA;
 NCBI_TaxID=10090;
 DISULFID
 Query Match
 PROPEP
 PROPEP
 090912
 CHAIN
 Matches
 RESULT 4
Q9D912
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 Zhao C., Nguyen T.:

Zhao C., Nguyen T.:

"cDNA cloning of three alpha-defensins and three demidefensins from "cpNA cloning of three alpha-defensins and three bone marrow.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Microbicidal activity against Gram-positive bacteria S. typhimurium S. aureus and L. monocytogenes, Gram-negative bacteria S. typhimurium and E.coli MLJ5 and fungi C.albicans and C. neoformans in vitro.

-!- SUBUNIT: Heterodimer of subunit A and subunit B linked by a disulfid bond at position 66 forming a cyclic RTD-1.

-!- TISSUE SPECIFICITY: Bone marrow; promyelocytes, myelocytes and mature neutrophils and monocytes.

-!- DEPLOPMENTAL STAGE: Expression and peptide accumulation starts
 Tanigami A., Sujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakemateu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nashikawa T., Kimura K., Wagatsuma M., Marakawa K., Kanehori K., Takahashi-Fujil A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Magai K., Isogai T., "NEDO human cDNA sequencing project.";

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Tang Y.-O., Yuan J., Osapay G., Osapay K., Tran D., Miller C.J., Ouellette A.J., Selsted M.E.,
"A Cyclic Antimicrobial Peptide Produced in Primate Leukocytes by the Ligation of Two Truncated alpha-Defensins.";
Science 286:498-502(1999).
 early during granulocytte myelopoiesis.
-!- MASS SPECTROMETRY: MW=2082.0; METHOD=MALDI.
-!- MISCELLANEOUS: The determined pI of this protein is greater than
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
 ñ
 SEQUENCE FROM N.A., SEQUENCE OF 65-73, AND MASS SPECTROMETRY.
TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99453140; PubMed=10521339;
 Length 243;
 0; Indels
 243 AA; 27566 MW; 23D41825EB9F782D CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Theta defensin-1, subunit B precursor (RTD-1).
 Score 60.5; DB 2;
Pred. No. 3.4;
2; Mismatches 0;
 76 AA.
 PRT:
 Macaca mulatta (Rhesus macaque)
 EMBL; AK131548; BAD18682.1; -.
 54.0%;
 177 VCQCLC---VCQCLC 188
 2 VCRCLCRRGVCRCLC 16
 Local Similarity 66.7 es 10; Conservative
 PRELIMINARY;
 Cercopithecinae; Macaca.
NCBI_TaxID=9544;
 ••
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Mammalia, Euther
NCBI_TaxID=9606;
 Name=RTD1A;
 Kinase.
SEQUENCE
 Query Match
 P82271
 Best Loca
Matches
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RESULT 3 P82271

SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20530913; PubMed=11076861;

-1- SIMILARITY: Belongs to the corticostatin/defensin family. EMBL; AF191101; AAF04390.1; -. EMBL; AF191103; AAF04392.1; -.

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mouse cDNA sequences.";
 AAH61079
 Query Match
 Q8CH20
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 RESULT 6
Q8CH20
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 AAH61079
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 Courable 12477932;

Characher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antschul S.F., Zeeberg B., Baretow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antschul M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Anting M., Madan A., Young A. Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A. Schwichenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Aizawa K., Atahira S., Fukuda S., Fukunishi Y., Furuno M., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H., A motani J., Kojima Y., Konno H., Kowa M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., A ckazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T., A Tejima Y., Toya T., Yammura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,

Submitted (Juu-2000) Leo the EMBL/GenBank/DDBJ databases.
 Gaps
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama T., Nishi K., Kitaunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yaliwake S., Inoue K., Togawa Y., Izawa M., Chara E., Matshika T., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matshiki M., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Sequencing sequence analysis (RISA) system-384-format sequencer enelysis (RISA) system-384-format genome Res. 10:1757-1771(2000)
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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 53.6%; Score 60; DB 2; Length 168; 56.2%; Pred. No. 2.9; tive 0; Mismatches 7; Indels
 l protein.
168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;
 Last sequence update)
Last annotation update)
 PRT; 168 AA.
 Created)
 MGD; MGI:1913992; 4931420D14Rik.
 18
 8
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Mus musculus (Mouse).
 3 CRCLCRRGVCRCLCRR
 66 скасанскаскасы
 PRELIMINARY;
 SEQUENCE FROM N.A. TISSUE=Testis;
 Hypothetical
 SEQUENCE
 Q6P8T4;
 Q6P8T4
 RESULT 5
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 Gaps
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 TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausherg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
 AAH61079;
14-APR-2004 (TEMBLrel. 27, Created)
14-APR-2004 (TEMBLrel. 27, Last sequence update)
14-APR-2004 (TEMBLrel. 27, Last annotation update)
14-APR-2004 (TEMBLrel. 27, Last annotation update)
Mypochetical protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 Length 168;
 / Match 51.8%; Score 58; DB 2; Length 168; Local Similarity 56.2%; Pred. No. 5.1; les 9; Conservative 0; Mismatches 7; Indels
 STRAIN-CD-1; TISSUB=Testis;

Xu X. Bai X., Silvius D., Becalier D., McFarland L., Xu X. Bai X., Silvius D., Becalier D., McFarland L., Xu X. Bai X., Silvius D., Benelle McC-2001 to the EMBL/GenBank/DDBJ databases.

EMBL; AF46350; AA015675.1;

MCD; MGI:1913992; 4931420D14Rik.

SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
 Indels
 Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC061079; AAH61079.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
 Q8CH20;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
8asic protein CKTIR3.
Name=4931420D148ik; Synonyms=Cktlr3;
Mus musculus (Mouse).
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 DB 2;
 51.8%; Score 58; DB 56.2%; Pred. No. 5.1; artive 0; Mismatches
 PRT;
 PRT;
 3 CRCLCRRGVCRCLCRR 18
 3 CRCLCRRGVCRCLCRR 18
 66 ckcccycrcckcccsk 81
 66 ckcccycrcckccsk 81
 Ouery Match
Best Local Similarity 56.27
Best Local 9, Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McZewan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouiffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Gones S.J., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
 SEQUENCE FROM N.A.
STRANIE-GYBL/GJ TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 Gaps
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
Hibrary, clone:4931420D14 product:hypothetical Cysteine-rich region
containing protein, full insert sequence.
Name-4931420D14Rik;
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
 .
 Score 58; DB 2; Length 168; Pred. No. 5.1;
 7; Indels
 Straubberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC061079; AAH61079.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUB=Testis;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 173 AA
 Mismatches
 PRT;
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
 ó
 51.8%;
 3 CRCLCRRGVCRCLCRR 18
 66 checeyerecekecesk 81
 Query Match
Best Local Similarity 56.22
Best Local 9; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 TISSUE=Testis;
 Q9D4K2;
 09D4K2
 RESULT 8
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SECURALS FROM N. T. ST. A ARABITAS S., Akimura T., Arai A., Aono H., Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Forno H., Carminoi P., Fukuda S., Fukunishi Y., Furino M., Hangaki T., Hara A., Hayatsu N., Hiranco K., Hiraoka T., Hori F., Inofini Y., Itoh M., Izawa M., Kasukawa T., Kato H., Imotani K., Ishii Y., Itoh M., Izawa M., Kaya S., Kurihara C., Awai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Osabel Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tajawa Y., Suinagawa A., Shiraki T., Tajawa Y., Suinagawa A., Shiraki T., Tajawa Y., Suinagawa R., Shiraki T., Rumamatsu M., Hayashizaki Y., Tagawa M., Takahashi F., Tanaka T., Muramatsu M., Hayashizaki Y., Too the EMBL/GenBank/DDBJ databases.

In Sumitted (Jul-2000) to the EMBL/GenBank/DDBJ databases.

In Shira K., Suina Y., Suina K., Suina K., Suina K., Shiraki Y., Mylishi AKOL6467; BABJO253.1; -
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 Gaps
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
0RFNames=C27A2.5;
CaenorabdAltis elegans.
CaenorabdAltis elegans.
Elukaryota; Metazoa; Nemacoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 STRAIN=C57BL/G1 TISSUB=Testis;
MEDLINE=C57BL/G1 TISSUB=1076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MAISTON H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakagudhi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa W., Tawa M., Ohara E., Watshiwaji K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Haysshizaki Y.,
Fugelone Res. 10:1757-1771(2000).
 .;
0
 C. elegans Sequencing Consortium.";
 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
 51.8%; Score 58; DB 2; Length 173;
56.2%; Pred. No. 5.2;
ive 0; Mismatches 7; Indels
 Hypothetical protein.
SEOUENCE 173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
 Ź
 188
 PRT;
 STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
 3 CRCLCRRGVCRCLCRR 18
 81
 CRCCCYCRCCRCCCSR
 9; Conservative
 PRELIMINARY;
 Best Local Similarity
 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Nhan M.;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=6239;
 Wilson R.;
 SEQUENCE
 Query Match
 Q18238.
 Matches
 RESULT 9
 Q18238
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Gaps
 Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
 / Match 50.9%; Score 57; DB 2; Length 166; Local Similarity 55.6%; Pred: No. 6.7; es 10; Conservative 0; Mismatches 8; Indels
 Ouery Match 50.9%; Score 57; DB 2; Length 164; Best Local Similarity 55.6%; Pred. No. 6.6; Matches 10; Conservative 0; Mismatches 8; Indels
 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, US5684, AAK68158.1; -.
HSSP; P10969; 1K7V.
 Anderson K., Chissoe S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein. - - SEQUENCE 166 AA; 16971 MW; 9D9D130351BB50F1 CRC64;
 Q17641 PRELIMINARY; PRT; 197 AA.
017641,
01-NOV-1996 (TEMBLEEL. 01, Created)
01-OCT-2001 (TEMBLEEL. 18, Last sequence update)
01-MAR-2004 (TEMBLEEL. 26, Last annotation update)
Hypothetical protein C04G6.7.
 Q95QY1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CO4G6.10.
ORFNames=CO4G6.10;
 WORMPETS COURSE 10; CE27649.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR006081; DEFENSIn_alpha.
InterPro; IPR006099; EGF 1ike.
InterPro; IPR001007; VWF_C.
INTERPROSITE; PS001094 4FE4S FERREDOXIN; UNKNOWN_1.
PROSITE; PS00209; DEFENSIN; UNKNOWN_1.
PROSITE; PS01209; VWFC_1; UNKNOWN_1.
 166 AA
 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
 97
 9
 1 GVCRCLCRRGVCRCLCRR 18
 1 GVCRCLCRRGVCRCLCRR 18
 80 GGCGCCCRPRCCCCCRR
 81 GCGCCCCRPRCCCCRR
 PRELIMINARY;
 SEQUENCE FROM N.A.
 STRAIN=Bristol N2;
 Wilson R.;
 Query Match
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Matches
 RESULT 12
Q17641
ID Q1764
AC Q1764
DT 01-NC
DT 01-NC
DT 01-MC
DT 01-MC
GN OKFNA
 RESULT 11
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 Gaps
 Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
 WormPep; C27A2.5; CE04105.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000552; P:defense response; IEA.

GO; GO:000651; P:referense response; IEA.

InterPro; IPR001450; P:re4S_ferredoxin.

InterPro; IPR0016081; Defensin_alpha.

InterPro; IPR001007; VWF.

PROSITE; PS001299; VFF4S_FERREDOXIN; UNKNOWN_1.

PROSITE; PS01209; VWFC_1; UNKNOWN_1.
 51.8%; Score 58; DB 2; Length 188;
55.6%; Pred. No. 5.6;
tive 0; Mismatches 8; Indels
 Sims M.A.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z66499; CAA91301.1; -.
PR; T24272; T24272.
HSSF; P10958; 2 CWG.
INTACt; Q22048; -.
 SEQUENCE FROM N.A.
STRAND-BATISTO N2;
WALCHSTON N2;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; 108766; AXX31463.1; -.
PIR; T15691; T15651.
HSRP; P10968; 2CWG.
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
 Hypothetical protein. - SEQUENCE 188 AA; 18878 MW; 0C5D0DC5CA8E0C4B CRC64;
 16499 MW; C002D48D36C9FCED CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
 WormPey, 70187,8; CE03592.
InterPro; IPR001450; Fee4S, ferredoxin.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR001007; WFF_C.
PR051TE; PS001289; 4FF4S, FERREDOXIN, UNKNOWN_1.
PR051TE; PS001289; DEFENSIN; UNKNOWN_1.
PR051TE; PS001208; NWFC_1; UNKNOWN_1.
PR051TE; PS01208; WFF_1; UNKNOWN_1.
 164 AA
 PRT;
 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
 1 GVCRCLCRRGVCRCLCRR 18
 81 GGGGCCCRPKCCCCRR 98
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 IntAct; Q18238;
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 Q22048
Q22048;
 RESULT 10
 022048
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274 AA; 28657 MW; AB547D9BD5470AE1 CRC64;
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 PRELIMINARY;
 PRELIMINARY;
 Local Similarity
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STRAIN=U1102;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10368;
 NCBI_TaxID=9606;
 Name=U88;
 SEQUENCE
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 Q69566
Q69566;
 09UI23;
 Q9UI23
 Matches
 RESULT 15
Q69566
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 Gaps
Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
 MEDLINE=21329048; PubMed=11435398;
MEDLINE=21329048; PubMed=11435398;
Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
Duesterhoeft A., Stiekem W., Entian K.D., Terryn N., Lemcke K.,
Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
Bevan M., Bancroft I.;
"Conservation of microstructure bewtween a sequenced region of the
genome of rice and multiple segments of the genome of Arabidopsis
 Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoldeae, Oryzeee, Oryza.
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 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
 WormPer 10909; 1802.

WormPer 10909; 1802.

InterPro: IPR001450; 4Fe4S ferredoxin.

InterPro: IPR001450; 4Fe4S ferredoxin.

InterPro: IPR001601; Defensin_alpha.

InterPro: IPR001007; WWF_C.

PROSITE; PS001096; 4Fe4S FERREDOXIN; UNKNOWN_1.

PROSITE; PS00022; EGF 1; UNKNOWN 1.

PROSITE; PS01208; VWFC_1; UNKNOWN 1.

PROSITE; PS01208; VWFC_1; UNKNOWN 1.

PROSITE: 1970 As, 20596 MW; FBSF9457BFB9B8AD CRC64;
 Query Match 50.9%; Score 57; DB 2; Length 197; Best Local Similarity 55.6%; Pred. No. 7.8; Matches 10; Conservative 0; Mismatches 8; Indels
 Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; U55554; AAK68161.1; -
HSSP; P10969; 1WGT.
 Anderson K., Chissoe S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
 0949G1 PRELIMINARY, PRT; 274 AA. 01949G1; 01-056-2001 (TrEWBLrel. 19, Created) 01-DEC-2001 (TrEWBLrel. 19, Last sequence update) 01-OCT-2003 (TrEWBLrel. 25, Last annotation update) Hypothetical protein ClSERIPDM.
 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
 Genome Res. 11:1167-1174(2001).
EMBL; AJ307662; CAC39030.1; -.
Gramene; Q949G1; -.
Hypothetical protein.
 1 GVCRCLCRRGVCRCLCRR 18
 82 GGGGCCCRPRCCCCRR 99
 SEQUENCE FROM N.A. STRAIN=Bristol N2;
 SEQUENCE FROM N.A. STRAIN=Bristol N2;
 NCBI_TaxID=4530;
 Wilson R.;
 thaliana.
 RESULT 13
 Q949G1
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 Gaps
 Littler E., Lawrence G., Liu M.Y., Barrell B.G., Arrand J.R., "Identification, cloning, and expression of the major capsid protein gene of human herpesvirus 6.";
J. Virol. 64:714-722(1990).
 Gaps
 Barrell B.G.; "Human herpesvirus 6 is closely related to human cytomegalovirus."; J. virol. 64:287-299(1990).
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 STRAIN=U1102;
MEDLINE=90080132; PubMed=2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
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 SEQUENCE FROM N.A.
TISSUB-Liver;
Zhang C., Liu W.Y., Zhang S., Duyang S., Luo L., Wei H., Zhou G.,
Zhang Y., Liu M., He F.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF11848; AF16687.1;
SEQUENCE 190 AA, 21480 MW; 4B8104A29AA33844 CRC64;
 50.4%; Score 56.5; DB 2; Length 190; 55.6%; Pred. No. 8.7;
Score 57; DB 2; Length 274;
Pred. No. 10;
 Indels
 6; Indels
 Human herpesvirus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 190 AA
Query Match

Social Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches
 2; Mismatches
 Created)
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MEDLINE=90112641; PubMed=2153237;
 Betaherpesvirinae; Roseolovirus.
 2 VCRCLCRRG---VCRCLC 16
 185 RCCCHRGCCRCRATR 199
 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, PRO0529.
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2002 (TrEMBLrel. 22,
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MEDLINE=93091236; PubMed=1333836;
 STRAIN=U1102;
MEDLINE=91333007; PubMed=1651403;
Teo 1.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
 Thomson B.J., Honess R.W.;
"The right end of the unique region of the genome of human herpesvirus 6 UlloZ contains a candidate immediate early gene enhancer and a momologue of the human cytomegalovirus US22 gene family.";
 SEQUENCE FROM N.A.
STRAIN-U1102;
STRAIN-U1102;
MEDLINE-9137459;
PARTIN M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
"Identification of a transactivating function mapping to the putative jumediate-early locus of human herpesvirus 6.";
J. Virol. 65:5381-5390(1991).
 STRAIN=U1102;
MEDLINE=22148942; PubMed=1310766;
Geng Y., Chandran B., Josephs S.F., Wood C.;
"Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type 1
MEDLINE=91226542; PubMed=1851252;
Thomson B.J., Eferathiou S., Honess R.W.;
"Arquisition of the human adeno-associated virus type-2 rep gene by
human herpesvirus type-6.";
Nature 351:78-80(1991).
 Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
"Identification of homologs to the human cytomegalovirus US22 gene
family in human helpesvirus-6";
J. Gen. Virol. 73:1661-1671(1992).
 Chang C.K., Balachandran N.; "Identification, and sequence analysis of a cDNA "Identification, characterization, and sequence analysis of a cDNA encoding a phosphoprotein of human herpesvirus 6."; J. Virol. 65:2884-2894
 STRAIN=U1102;
MEDLINE=92266671; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human
 Ellinger K., Neipel F., Foa-Tomasi L., Campadelli-Fiume G., Fleckenstein B.;
 "The glycoprotein B homologue of human herpesvirus 6.";
J. Gen. Virol. 74:495-500(1993).
 MEDLINE=92333248; PubMed=1321205;
 STRAIN=U1102;
MEDLINE=92333249; PubMed=1321206;
 MEDLINE=91237802; PubMed=1851860;
 STRAIN=U1102;
MEDLINE=93187613; PubMed=8383182;
 Virol. 66:3918-3924 (1992)
 Virol. 66:1564-1570(1992)
 SEQUENCE FROM N.A.
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 STRAIN=U1102;
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MEDLINE=93389439; PubMed=8397282;
Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
"Identification and expression of the human herpesvirus 6 glycoprotein
H and interaction with an accessory 40K glycoprotein.";
J. Gen. Virol. 74:1847-1857(1993).
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 STRAIN=U1102;
MEDLINE=93224882; PubMed=8385692;
Gompels U.A., Carrigan D.R., Carss A.L., Arno J.;
Gompels U.A., Carrigan D.R., Carss A.L., Arno J.;
I"Two groups of human herpesvirus 6 identified by sequence analyses of laboratory strains and variants from Hodgkin's lymphoma and bone
 STRAIN=U1102;
MEDLINE=3331710; PubMed=7687803;
MEDLINE=3331710; PubMed=7687803;
Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E., Greenamoyer C., Dambaugh T.R.;
"A strongly immunoractive virion protein of human herpesvirus 6
"A strongly immunoractive virion protein of human herpesvirus 6
and mapping of a variant-specific monoclonal antibody reactive
 Jones M., Teo I.;
"Identification and analysis of the transport/capsid assembly protein (tp/cap) gene of human herpesvirus-6 (HHV-6).";
Virology 197:449-454(1993).
Gompels U.A., Carss A.L., Sun N., Arrand J.R.; Infectivity determinants encoded in a conserved gene block of human
 MEDINE-94118404; PubMed=8289364;
Nicholas J., Martin M.;
Nicholas J., Martin M.;
"Nuclectide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpsvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions.";
J. Virol. 68:597-610(1994).
 ŝ
 MEDIJUE=91181269; PubMed=8134119;
Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z., Frenkel N., Rosenthal L.J.;
A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates HIV-1.";
Oncogene 9:1167-1175(1994).
 "Identification and mapping of the gene encoding the glycoprotein complex gp82-gp105 of human herpesvirus 6 and mapping of the neutralizing epitope recognized by monoclonal antibodies."; j. virol. 67:4611-4620(1993).
 Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong
 MEDLINE=93323202; PubMed=7687301;
 MEDLINE=94025598; PubMed=8212582;
 STRAIN=U1102;
MEDLINE=94167865; PubMed=8122364;
 marrow transplant patients.";
J. Gen. Virol. 74:613-622(1993).
 irology 195:521-531(1993)
 DNA Seq. 3:25-39(1992)
 SEQUENCE FROM N.A.
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FROM N.A.
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 NCBI_TaxID=10116;
 TISSUE=Thalamus;
 28
 AAR24072;
 SECUENCE
 Receptor
 SEQUÊNCE
 AAR24072
 06ZQS2
 RESULT 18
Q6ZQS2
 RESULT 19
BAC87611
 RESULT 17
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 1;
Zhou Y., Chang C.K., Qian G., Chandran B., Wood C.; "trans-activation of the HIV promoter by a cDNA and its genomic clones of human herpesvirus-6."; virology 199:311-322(1994).
 9
 Thomson B.J., Dewhurst S., Gray D., "Structure and heterogeneity of the a sequences of human herpesvirus strain variants U1102 and Z29 and identification of human telomeric repeat sequences at the genemic termini.", Virol. 68:3007-3014(1994).
 Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
Goballie S., Aunis D., Maitre M.;
"Cloning and characterization of a rat brain receptor that binds the
endogenous neuromodulator gamma-hydroxybutyrate.";
PASEB J. 0.0-0(2004).

EMBL; AY46593; AAR4072.1; -.
EMBL; AY46593; Pireceptor activity; IEA.
InterPro; IPR0081209; Ribosomal S14.
InterPro; IPR0081209; Ribosomal S14.
InterPro; IPR0081301; Transmem 4.
Pfam; PR00315; Tetraspanin.
PRINTS; PR00315; Tetraspanin; I.
PRINTS; PR00315; Tetraspanin; I.
PRINTS; PR00315; Tetraspanin; I.
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 Gaps
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 MEDLINE-95146989; PubMed=7844567;
Gompels U.A., Macaulay H.A.;
"Characterisation of human telomeric repeat sequences from human
herpesvirus-6 and relationship to replication.";
J. Gen. Virol. 76:451-458(1995).
 3;
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 Length 413;
 Length 512;
 2; Indels
 Indels
 512 AA; 56146 MW; 44DD12B937C40D60 CRC64;
 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
 49.6%; Score 55.5; DB 2;
64.7%; Pred. No. 28;
tive 1; Mismatches 4;
 DB 2;
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0; Mismatches
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 Gamma-hydroxybutyrate receptor.
 385 VCVCVCVR-VCLCLCVR 400
 2 VCRCLCRRGVCRCLCRR 18
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Matches 10; Conservative (
 123 vcacic---vcacic 134
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 STRAIN=U1102;
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 SEQUENCE
 Receptor
 Query Match
 Q6RY99
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Matches
 RESULT 16
Q6RY99
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 Kanehori K., Watanabe S., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK128797; BAC87611.1; -.
EMBL; AK128797; BGF 2; UNXNOWN 1.
EROSITE; PSO1186; EGF 2; UNXNOWN 1.
EROSITE; PSO1186; EGF 2; UNXNOWN 1.
 Gaps
 STRAIN-Wistar; TISSUE-Hippocampus; Andilar C., Humbert J.P., Andilamampandry C., Taleb O., Viry S., Muller C., Humbert J.P., Taleb O., Viry B., Muller B., Annis D., Maitre M.; "Cloning and characterization of a rat brain receptor that binds the endogenous neuromodulator gamma-hydroxybutyrate."; EASEB J. 0:0-0(2004).

EMBL; AY485933; AAR24072.1; -.
 Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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 Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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 ;
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 Length 512;
 Score 55, DB 2; Length 201;
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2; Mismatches 5; Indels
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 02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
 Q6ZQS2;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheitcal protein FLJ45585.
Homo sapiens (Human).
 49.6%; Score 55.5; DB 2;
64.7%; Pred. No. 28;
ive 1; Mismatches 4;
 512 AA
 201 AA
 PRT:
 Gamma-hydroxybutyrate receptor.
 385 VCVCVCVR-VCLCLCVR 400
 2 VCRCLCRRGVCRCLCRR 18
 49.1%;
53.3%;
 | | | : | | | | : | VCLCVCLCVC 72
 Query Match
Best Local Similarity 64...
Thes 11; Conservative
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Best Local Similarity 53...
Best Academic Strong Stro
PRELIMINARY;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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 Gaps
 Gaps
 Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Champe M., Conzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BTO0129; ANN11054.1; -
Flybase; FBDR0051029; CG31029.

SEQUENCE 905 AA; 102573 MW; 301303CE74E9D29E CRC64;
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 ;
0
 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopteray, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
 Kershaw J.K.;
Submitted (NOV-1996) to the EWBL/GenBank/DDBJ databases.
Submitted (NOV-1996) to the EWBL/GenBank/DDBJ databases.
EMBL; Z81579; CAE17915.1;
InterPro; IPRO1010450; 4Fe4S ferredoxin.
InterPro; IPRO10107; VWFC.
InterPro; IPRO10107; VWFC.
INTERPRO; PROSITE; PS01028; 4FF4S FERREDOXIN; UNKNOWN 1.
PROSITE; PS01028; 4WPC-1; UNKNOWN 1.
PROSITE; PS011208; VWPC-1; UNKNOWN 1.
PHypothetical protein.
SEQUENCE 212 AA; 22857 MW; 22F62CE4073CCA4E CRC64;
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48.2%; Score 54; DB 2; Length 212;
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Matches 9; Conservative 0; Mismatches 7; Indels
01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein R13H4.8.
 Last sequence update)
Last annotation update)
 905 AA
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Name=CG2164; ORFNames=CG31029;
 1 GVCRCLCRRGVCRCLCR 17
 3 CRCLCRRGVCRCLCRR 18
 84 CGCCCCRPRCCCCRR 99
 01-MAR-2003 (TremBlrel, 23, 01-MAR-2003 (TremBlrel, 23, 01-MAR-2004 (TremBlrel, 26,
 Science 282:2012-2018(1998).
 PRELIMINARY;
 Caenorhabditis elegans.
 investigating biology
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A. STRAIN=Bristol N2;
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 SEQUENCE
 QBIHD6;
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Matches
 RESULT 22
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 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arrhropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
 Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAABO1000199; EAA45966.1; -.
 48.7%; Score 54.5; DB 2; Length 212; 60.0%; Pred. No. 17;
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 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGE0000024926 (Fragment).
 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FL-45585 fis, clone BRTHA3013882.
Homo sapiens (Human)
 212 AA.
 201 AA
 212 AA
 1; Mismatches
 01-OCT-2003 (TrEMBLrel. 25, Created)
 PRT;
 PRT;
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58 VCLCVCLVSVCLCVC 72
 2 VCRCLCRRGVCRCLC 16
 3 CRCLCRRGVCRCLCR 17
 33 CRCRCQ---CRCRCR 44
 Local Similarity 60.0
nes 9; Conservative
 · PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
 [1]
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 NCBI_TaxID=9606;
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 BAC87611
BAC87611;
 SEQUENCE
 Query Match
 Q7YWV7;
 Q7YWV7
 Q7PDW6
 Best Loc
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 RESULT 20
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RAMEDLINE-20196006; PubMed=10731132;
RADAINERE KANN R.W.
REDLINE-20196006; PubMed=10731132;
RADAINE-20196006; PubMed=10731132;
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RADAINE-20196006; PubMed=10731132;
RADAINERE R.A. Levis S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.G., Mortman J.R., Paradell M.D., Zhango Q., Chen L.K.,
RADAINER R.A. Levis S.E., Richards R.G., Champe M., Pfeinfer B.D.,
RADAINER R.M., Bancer E.G., Helt G., Nelson C.R., Gabor G.L.,
RADAIL J.F., Agbayani A., Paradieves-Péannécoh C.R., Gabor G.L.,
RADAIL J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benckova D., Boccham M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Boccham M.R., Bouck J., Brokstein P., Brottler P.,
RADAINER R.M., Cawley S., Dahlke C., Davenpour L.B., Cherer A., Chandra I.,
RADAINER R.J., Downes M., Deng Z., Mays A.D., Dew I., Davies P.,
Durbin K.J., Belos P.V., Bernan B.P., Brottler S., Dunkov B.C., Dunn P.,
RADAINER R.J., Belos B., Delcher A., Deng Z., Mays A.D., Dew I., Davies P.,
RADAINER R.J., Belos P.V., Howland T.J., Hernandez J.R., Fleischmann W.,
RADAINER R.J., Gabriellan A.E., Garry N.S., Gelbart W.M., Glasser K.,
Adalain M., Kalush F., Kapen G.H., Ke Z., Guban P., Harris M.,
Adalain M., Kalush F., Kapen G.H., Ke Z., Guban P., Harris M.,
Lasko P., Lei Y., Levitsky A.A., Li J., Wei M.H., Ibegwan C.,
RADAIL R.M. Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,
Radien B.E., Kodirez C.D., Kraft C., Mortis J., Moshrefi A.,
Runt S.M., Moyn W., Murphy B., Murphy L., Murany D.M., Nelson D.K.,
Runt S.M., Woldser C.D., Rad C., Schelber F., Smith T.,
Shiekas R., Rediract K., Patanos I., Simpleron R., Stupe D., Smith T.,
Runt S., Wassarman D.A., Weinscon M., Strong R., Sun E.,
Striskas R., Woodager, Worley X., Zhou S., Zhou S.
 MEDLINE=22436065, PubMed=12537568,
MEDLINE=22436065, PubMed=12537568,
MEDLINE=22436065, PubMed=12537568,
MEDLINE=22436065, PubMed=12537568,
Datel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
Batel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A. Laverty T., Muzny D.M., Nelson C.R.,
Pacifer B.D., Richards S., Sodergren E.J.,
Weinstas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
 Created)
Last sequence update)
Last annotation update)
 905 AA
 PRT.;
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MEDLINE=22426070; PubMed=12537573;
728 GFAPCTCRRPVASCFCR 744
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
 PRELIMINARY;
 SEQUENCE FROM N.A.
 CG31029-PA.
ORFNames=CG31029;
 NCBI_TaxID=7227;
 QBIMJ2;
 Q8IMJ2
 RESULT 23
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KEDINE=21388257; PubMed=1247932;

KEDINE=21388257; PubMed=1247932;

KILL Shemmen C.M.; Schuler G.D.;

KILL STAIN=BAT INSCHULER F.S.; Wagner L., Shemmen C.M.; Schuler G.D.;

KALAUSPER R.D.; Collins F.S.; Wagner L., Shemmen C.M.; Schuler G.D.;

Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H., Moore T., Max S.I.; Wang J., Hsieh F.;

A piatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

Rapleton M., Soares M.B.; Bonaldo M.F.; Casavant T.D.; Scheetz T.E.;

Rapleton M.J.; Usdin T.B.; Toshlyvki S., Carninci P.; Prange C.,

Rapleton M.J.; Usdin T.B.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Raples S., Morley K.C.; Halle S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

Richards S., Worley K.C.; Halle S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

Nillalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X., Gibbs R.A.;

Fahey J.J.; Helton E.; Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C.; Shevchenko Y.; Bouffard G.G.;

Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fitise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., The Company of the Drosophila melanogaster euchromatin: "The transposable elements of the Drosophila melanogaster euchromatin:
 Gaps
 SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Fradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
 Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: a
 0
 48.2%; Score 54; DB 2; Length 905; 52.9%; Pred. No. 70;
 8; Indels
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003772; AAN14217.1; -.
 59471B320E041C20 CRC64;
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein zgc:63759.
Name=zgc:63759;
 Genome Biol 3: RESEARCH0083-RESEARCH0083 (2002).
 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 0; Mismatches
 FlyBase; FBGn0051029; CG31029.
SEQUENCE 905 AA; 102461 MW;
 728 GFAPCTCRRPVASCFCR 744
 1 GVCRCLCRRGVCRCLCR 17
 Query Match
Best Local Similarity 52.9.
...hes 9; Conservative
 PRELIMINARY;
 genomics perspective.
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 IntAct; Q8IMJ2;
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=98167900; PubMed=9435294;
Bichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression pattern and stimulation
of the differentiation of VEGFR2 expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
vascular endothelial growth factor C.; 099BFCC79151BF2B CRC64;
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C -1- SIMILIARITY: Belongs to the PDGF/VEGF growth factor family.

EMBL; VISB37; CAA75799.1; -.

R HSSP; P49763; 1PZV.

R GO, GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016021; F:growth factor activity; IEA.

R GO; GO:000813; F:growth factor activity. IEA.

R InterPro; IPR004153; CXCXC_repeat.

R InterPro; IPR004153; CXCXC_repeat.

R InterPro; IPR00405400; GP_CYEKNOT.

R Pfam; PF00341; PDGF; 1.

R PFAM; PF00341; PDGF; 1.

R PRINTS; PR00448; GFCYSKNOT.

R PRODOM; P0001659; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                      Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055236; AHR55236.1; -.
InterPro; IRN002172; LDL receptor_A.
Pfam; PF00057; Ldl recept_a; 6.
SMART; SM00192; LDLa, 6.
PROSITE; PS50068; LDLRA 1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein. 379 AA; 40591 MW; D763CB41A9F752C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            057352;
01-UTM-1998 (TrEMBLrel. 06, Created)
01-UTM-1998 (TrEMBLrel. 06, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor C precursor.
                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 47.8%; Score 53.5; D
Local Similarity 45.5%; Pred. No. 38;
hes 10; Conservative 2; Mismatches
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PROSITE; PS50278; PDGF 2; 1.
Growth factor; Mitogen; Signal.
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STRAIN-AB; IISSUE-Whole body;
Strausberg R.;
                                                                                                                            and mouse cDNA sequences."
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418 AA;
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SEQUENCE 37
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Kausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Atlanener R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Osdres M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loguellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gabbs R.A.,
A Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A., AND SEQUENCE OF 103-120.
MEDLINES 96179224; PubMed=861704;
Joukov V., Pajusola K., Kaippainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinen N., Alitalo K.;
A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
EMBO J. 15:290-298(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor protein) (VRP) (Flt4 ligand) (Flt4-
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96203094; PubMed=8612600;
Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk
Saksela O., Kalkkinen N., Alitalo K.;
EMSO J. 15:1751-1751(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Glial tumor;
MEDLINE-96312526; PubMed-8700872;
Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
"Vascular endothelial growth factor-related protein: a ligand
specific activator of the tyrosine kinase receptor Flt4.";
Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
47.8%; Score 53.5; DB 2; Length 418; 26.7%; Pred. No. 41; ive 6; Mismatches 1; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                           419 AA.
                                                                                                                                                                                                290 COCVCKGGVRPISCGPHKELDRASCQCMCK 319
                                                                                                                                                 3 CRCLCRRGV-----CRCLCR 17
Query Match
Best Local Similarity 26.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Barra M.A., Schein J.E., Jones G.M., Marra M.A., Weneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                   SEQUENCE OF 32-41; 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227. MEDLINE=97377029; PubMed=2233800; Joukov V., Sorsa T., Kumar V., Jeltsch M., Claesson-Welsh L., Cao Y., Saksala O., Kalkkinen N., Alitalo K.; "Proteolytic processing regulates receptor specificity and activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 053111; AAR025091; ...

R EMBL; 058111; AAR025091; ...

R PIR; 56207; 86207.

R FSP; P49763; 1F2V.

R Genew; HGNC:12682; VEGFC.

R MIM; 601528; ...

R GO; GO:0007515; P:1ymph gland development; TAS.

GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007515; P:1ymph gland development; TAS.

R GO; GO:0007517; P:1ymph gland development; TAS.

R ThterPro; IPR00415; CXCXC repeat.

R InterPro; IPR00407; P:1ymph gland; PF031128; CXCXC; F:1ymph glan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0438; GFCYSKNOT.
ProDom; PD001629; PD growth_factor; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X94216; CAA63907.1; -.
EMBL; U431142; AAA85214.1; -.
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By similarity.
By similarity.
By similarity.
Interchain (By similarity).
Interchain (By similarity).
Intend (GLNAc. . ) (Potential).
N-linked (GLNAc. . ) (Potential).
N-linked (GLNAc. . ) (Potential).
R-5: No proteolytic processing and lower effect on VEGRP-2 and VEGFP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Angiogenesis; Cleavage on pair of basic residues;
Direct protein sequencing, Glycoprotein; Growth factor; Mitogen;
Multigene family; Repeat; Signal.
SIGNAL 1 31 Or 102.
                                                                                  Or 102.
Vascular endothelial growth factor
                                                                                                                                    4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to the PDGF/VEGF growth factor family. EMBL; CR541897; CAG46695.1; ---
InterPro; IPR004163; CXCXC, repeat.
InterPro; IPR002400; GF CySknot.
InterPro; IPR000072; PD-growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 47.8%; Score 53.5; DB 2; Length 419; Local Similarity 26.7%; Pred. No. 41; les 8; Conservative 6; Mismatches 1; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46943 MW; 9F598703C13E1B55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 41;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CRCLCRRGV-----CRCLCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.5;
Pred. No. 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03128; CXCXC; 4.
Pfam; PF00341; PDGF; 1.
PRINTS, PR00438; GFCYSKNOT.
ProDom; PD001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           46883 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%; 26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 1
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Guery Coal Similarity 26.77,
Best Local Similarity 26.77,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                    111
227
419
362
                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                           419 AA;
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228
280
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                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                               DISULFID
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Best Local 8
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                                                                                                   CHAIN
PROPEP
DOMAIN
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                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
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Q6FH59
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-- CRCLCR 17

3 CRCLCRRGV----

|:|:|| |: CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320

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A MEDLINE=22388257; PubMed=12477912;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlausner R.D., Collins F.S., Wagner L., Sheafer C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rabin G.W., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carnhol P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carnhol P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garden R.D., Dickson M.C., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A. Jones S.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
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PubMed=14702039;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
SMBL; BCG6565; AAH65685.1; -.
SEQUENCE 419 AA; 46883 WW; 9F598719DB3E014F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ12547.
Homo sapiens (Human).
                                                                              02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
VGC-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Vascular endothelial growth factor C preproprotein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                              02-MAR-2004 (TrEMBLrel. 27, Created)
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26./*
Best Local 8; Conservative
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                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Bladder;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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                        AAH63685
                                          AAH63685
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AAH63685
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Yamamoto J., Saito K., Kawai Y., Isono Y., Makamira Y., Nagahari K., Ra Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K., Fujimori K., Anatanabe M., Hiraoka S., Chiba Y., Ishidashi Fulii A., Hara H., Murakawa K., Fujimori K., Ramanori K., Takiqueli S., Watanabe S., Yosida M., Hotuta T., Kusano J., RA Kanachori K., Takidashi-Fulii A., Hara H., Tanase T., Nomura Y., RA Kanachori K., Takidashi-Fulii A., Hara H., Tanase T., Nomura Y., RA Kanachori K., Takinawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Ayoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., RA Wasaahino K., Yuuki H., Oshima A., Sasaki N., Tarahima Y., Salimizu T., Wakebe H., RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukurumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Watanabe K., Kumagai A., Itakura S., Fukurumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Natanabe K., Kumagai A., Itakura S., Fukurumi Y., Ramamura K., Nakatima Y., Matano T., Noguchi S., Itoh T., Shigeta K., Senba T., Rayabata A., Hikiji T., Kobatake N., Inagaki H., Natanabe T., Sugano J., Satoh T., Shigeta K., Saakami T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K., Rayabata S., Nakajima Y., Marano T., Markali M., Saokaki M., Nakajawa K., Nakajawa Y., Nakajawa Y., Nakajawa Y., Nakajawa Y., Nakajima Y., Ohara O., Isogai T.,
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A Mark H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             f match 47.3%; Score 53; DB 2; Length 307; Local Similarity 57.9%; Pred. No. 36; les 11; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
BMBL; AK022609; BAB14128.1; -.
SEQUENCE 307 AA; 32780 MW; 4CC18ACD39BD3AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 VCGCLCVCGAHLCVCVCLC 134
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01-UUN-2003 (TrEMBLrel. 24,
01-WAR-2004 (TrEMBLrel. 26,
02086-PB.
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Matches
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Probler K.O. Evagealists C.C. Ferrac. S. Perises. S. Peastechmann H.,

Rodoler A., Gong F. Gorrell I.H. Gu Z. Gans P., Harris M.,

Radiali M., Marvey D., Heisman T.J., Hernandez J.R., Houck J.,

Radiali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

Adaili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

Radiali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

Radiali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

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Radiali M., Koy M., Marphy B., Marphy L., Marphy D.H., Marbarson J.H.,

Radiason D.R., Nelson K.A., Markon K., Nakon K., Nakon D.H.,

Radiason D.R., Nelson K.A., Markon K., Nakon K., Suched B.H.,

Radiason D.R., Nelson K.A., Markon K., Marbary L., Marny D.H., Marbar D.L.,

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Radiason B.R., Markon B.R., Markon B.R., Markon B.R., Markon B.R.,

Radiason B.R., Markon B.R., Markon B.R., Markon B.R., Markon B.R.,

Radiason B.R., Markon B.R., Markon B.R., Markon B.R.,

Radiason B.R., Markon B.R
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Gaps
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EVBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is nererve; IPR000152; Asx. hydroxyl_S.

R InterPro; IPR000152; Asx. hydroxyl_S.

InterPro; IPR000159; EGF_2.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR001791; Sushi_SCR_CCP.

R InterPro; IPR000436; Sushi_SCR_CCP.

R Pfam; PF00008; EGF_5.

R Pfam; PF00054; Pentaxin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                         2; Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1823 AA; 200582 MW; 5740C4C700804379 CRC64;
                                                                                                                                                                                                                                                                                             96380 MW; 52196D164F52F5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1823 AA.
                                                                                                                                                                                                                                                                                                                                                   11arity 64.3%; Pred. No. 91;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00453; VWFADOMAIN.
ProDom; PD002153; Pentaxin, 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
                     Ffam; PF00008; EGF; 1.
PFAm; PF00008; Laminin. EGF; 6.
PRINTS; PR00011; EGFLAMINN.
SMART; SM00180; EGF_Lam; 3.
PROSTIE; PS00108; EGF_1; 11.
PROSTIE; PS01186; EGF_2; 13.
PROSTIE; PS0026; EGF_2; 13.
PROSTIE; PS0026; EGF_3; 7.
Laminin EGF-1ike domain.
SEQUENCE 881 AA; 96380 MW; 52196D16
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PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50026; EGF_3; 5.
PROSITE; PS50025; HYR; 2.
PROSITE; PS50025; HAM G DCMAIN; 1.
PROSITE; PS50018; PA2_HTS; UNKNOWN_1.
PROSITE; PS50923; SUSHI; 8.
ROSITE; PS50934; VWFA; 1.
NOW TER 1823 1823
SEQUENCE 1823 AA; 200582 MW; 5740
InterPro; IPR002049; Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
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Pfam; PF00092; VWA; 1.
PRINTS; PR00895; PENTAXIN.
PRINTS; PR00453; VWFADOWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ENSANGG00000016557
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENSANGP00000019046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=180454;
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Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690(2001).
 Q6R5G9
 RESULT 34
 Q6R5G9
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 MEDLINE=22799168; PubMed=12907728;

MEDLINE=22799168; PubMed=12907728;

BI-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaud F.,

BI-Tarkin C., Wanless D., Peterson J., Hou.L., Taylor S., Twedie A.,

Biteau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E.,

Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,

Van Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,

A Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,

A Adams M.D., Fraser C.M., Donelson J.E.;

"The sequence and analysis of Trypanosoma brucei chromosome II.";

Nucleic Acids Res. 31:4856-4863(2003).

"Phypothetical protein."
 Gaps
 Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma
NCBI_TaxID=5691;
 Gaps
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630032M05 product:hypothetical protein, full insert
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 ö
 Query Match

46.9%; Score 52.5; DB 2; Length 101;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 2; Indels 3
 Length 1823;
 6; Indels
 l protein.
101 AA; 10880 MW; E63D8E62A9CA6748 CRC64;
 Created)
Last sequence update)
Last annotation update)
 47.3%; Score 53; DB 2; 56.2%; Pred. No. 1.7e+02; ive 1; Mismatches 6
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STRAIN=C57BL/63; TISSUE-Thymus;
MEDLINE=99279233; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 118 AA.
 101 AA
 STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTium;
 PRT;
 PRT;
 262 VCSCLTTSGHYRCICK 277
 16
 4 GVCVCVC---VCVCVC 16
 2 VCRCLCRRGVCRCLCR 17
 01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
 1 GVCRCLCRRGVCRCLC
 Query Match
Best Local Similarity 56.2
Matches 9; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Hypothetical protein.
ORFNames=Tb927.2.4940;
 Mus musculus (Mouse)
 Trypanosoma brucei.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 sequence.
 Q8C9N2
 07YUU2
 RESULT 33
Q8C9N2
 RESULT 32
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi U. Aizawa K., Akimurar., Arakawa T., Bono H., Carninci P., Adachi U., Aizawa K., Akimurar., Arakawa T., Harbizume W., Arakabida S., Furuno M., Haragoki T., Haraka T., Hirozane T., A Hayashida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowia M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nomira K., Nomira K., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinaka K., Shiraki T., Sogabe Y., Tanaka T., Agawa A., Takabashi F., Takaku-Akahira S., Takeda Y., Tanaka T., A Tagawa M., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (Jul-2001) to the BEL/GenBank/DDBJ databases.
 SECUENCE FROM N.A.
STRAIR-CAPEL/GJ; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of Cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
Nature 420:563-573(2002).
 Tagami M.,
 Gaps
 STRAIN=CS7BL/6J; TISSUE=Thymus;
STRAIN=CS7BL/6J; TISSUE=Thymus;
STRAIN=CS7BL/6J; TISSUE=Thymus;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Miramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIFE integrated Sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
 ĢēRSG9;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 3,
 46.9%; Score 52.5; DB 2; Length 118; 56.2%; Pred. No. 18; 2; Indels ive 2; Mismatches 2; Indels
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PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
Hypothetical protein.
BRQUENCE 118 AA; 13452 MW; CA98EICGB01CD77F CRC64;
 133 AA.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
 1 GVCRCLCRRGVCRCLC 16
 63
 Query Match
Best Local Similarity 50...
9, Conservative
 PRELIMINARY;
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us-10-009-317a-33.rup

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product:hypothetical protein, full insert sequence.
 9; Conservative
 Query Match
Best Local Similarity
Matches 9; Conserv
 1;
 STRAIN-C57BL/6J;
Sharov A.A., Piao Y., Matoba R., Dudekula D.B., Qian Y., VanBuren V.,
Sharov A.A., Piao Y., Stagg C.A., Bassey U.C., Wang Y., Carter M.G.,
Hamatani T., Aiba K., Akutsu H., Sharova L., Tanaka T.S., Kimber W.L.,
Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R.,
Taub D., Hodes R.J., Longo D.L., Schlessinger D., Keller J., Klotz E.,
Kelsoe G., Umezawa A., Vescovi A.L., Rossant J., Kunath T.,
Hogan B.L., Curci A., D'Urso M., Kelso J., Hide W., Ko M.S.;
HTranscriptome analysis of mouse stem cells and early embryos.";
 Sharov A.A., Piao Y., Matoba R., Dudekula D.B., Qian Y., VanBuren V., Falco G., Martin P.R., Stagg C.A., Basesy U.C., Wang Y., Carter M.G., Falco G., Martin P.R., Akuteu H., Sharova L., Tanaka T.S., Kimber W.L., Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R., Taub D., Hodes R.J., Longo D.L., Schlessinger D., Keller J., Klotz E., Hogan B.L., Curci A., Vescovi A.L., Rossant J., Kunath T., Hogan B.L., Curci A., D'Urso M., Kelso J., Hide W., Ko M.S.; Transcriptome analysis of mouse stem cells and early embryos."; EMBL, AY512913; AAR87784.1; -.
 Gaps
 Gaps
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)
Mus musculus 11 days pregnant adult female ovary and uterus CDNA,
RIKEN full-length enriched library, clone:5031438A03
 ÷
 3;
 46.9%; Score 52.5; DB 2; Length 133; 60.0%; Pred. No. 20; ive 1; Mismatches 2; Indels
 2; Length 133;
 2; Indels
 Hypothetical protein.
SEQUENCE 133 AA; 14583 MW; 5929328D1A4B4BF7 CRC64;
 14583 MW; 5929328D1A4B4BF7 CRC64;
 Created)
Last sequence update)
Last annotation update)
 80
 ; Score 52.5; DE; Pred. No. 20; 1; Mismatches
 133 AA
 PRT;
 PRT;
 PLOS Biol. 1:410-419(2003).
EMBL; AY512913; AAR87784.1; -.
 46.9%;
 20-MAY-2004 (TrEMBLrel. 27, 20-MAY-2004 (TrEMBLrel. 27, 20-MAY-2004 (TrEMBLrel. 27, Hypochetical protein. Mus musculus (Mouse).
 ilarity 60.0%;
Conservative
 2 VCRCLCRRGVCRCLC 16
 57 VCMCLC---VCLCVC 68
 2 VCRCLCRRGVCRCLC 16
 57 VCMCLC---VCLCVC 68
 9; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Hypothetical protein.
SEOUENCE 133 AA; 1,
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
Matches 9; Conserv
 FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6J;
 AAR87784;
 SEQUENCE
 AAR87784
 OBBPC0;
 QBBPC0
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Q8BPC0
 AAR87784
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CSTRAIN-C57BL/60; TISSUB-Ovary and uterus;

RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizowe W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imoteni K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Katihara C., Matsayama T., Miyazaki A., Murata M., Nakamura M.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Taqami M.,

RA Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

R. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

RW Hypothetical protein.

SQUENCE 146 AA; 16179 MW; 711E0C93BCBODBBB CRC64;
 SECUENCE FROM N.A.
STRANIE-STBL/G17 IISSUE=Ovary and uterus;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thailysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:563-573 (2002).
 MEDLINE-20499974; PubMed=11042155; Carninci P., Shibata K., Itoh M., Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Nuramatization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 Gaps
 SEQUENCE FROM N.A.
STRAIN-G7SPB1/64); TISSUE-Ovary and uterus;
STRAIN-G7SPB1/64); PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama V., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Cokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 ۳.
 Length 146;
 Indels
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 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB=Ovary and uterus;
MEDLINE=99279253; Pubmed=10349636;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 DB
 46.9%; Score 52.5; D 52.9%; Pred. No. 22; tive 2; Mismatches
 SEQUENCE FROM N.A.
TRAIN=CSPL6/G1, TISSUE=OVARY and uterus;
MEDLINE=11085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
 SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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[2]
SEQUENCE FROM N.A.
TISSUE=Whole;
 STRAIN-Bristol N2;
 SEQUENCE FROM N.A
 NCBI_TaxID=6239;
 SEQUENCE
 Query Match
 QBIRLO
QBIRLO;
 29XVX3;
 Q9XVX3
 RESULT 40
QBIRLO
ID QBIRLO
AC QBIRLO
 Best Loca
Matches
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 A CONTRACTOR OF THE CONTRACTOR
 MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MAISCALL S.P., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Morer, Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Woffernan K.J., Malek J.A., Gunstane P.H.,

Richards S., Morley K.C., Hale S., Garcie S., Garcie P.H.,

Richards S., Morley K.C., Hale S., Garcie S.J., Lu X., Gibbs R.A.,

Richards S., Morley K.C., Hale S., Garcie B.D., Dickson M.C.,

Rahe J., Halton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Minish M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"The desire of the sci. U.S.A., 199:16993(2002).
 .;
 SEQUENCE FROM N.A.
TISSUB-Human small intestine;
TISSUB-Human small intestine;
TISSUB-Human small intestine;
Watanaba K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO26249; BAB15412.1; -
SEQUENCE 160 AA; 16738 MM; FBBB34293CBEZTET CRC64;
 Gaps
 Brachydanio rerio (Zebrafísh) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Weopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ225596.
Hypothetical protein FLJ225596.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 'n
 Query Match
Best Local Similarity 56.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 2; Indels
 Q6GQP2 PRELIMINARY, PRT, 462 AA.
Q6GQP2,
Q5GJD2,
Q5-JUL-2004 (TrEMELrel. 27, Created)
O5-JUL-2004 (TrEMELrel. 27, Last sequence update)
05-JUL-2004 (TrEMELrel. 27, Last annotation update)
Hypothetical protein (Fragment)
 PRT; 160 AA.
 96 VCMCVC---VCVCVCMR 109
2 VCRCLCRRGVCRCLCRR 18
 1 GVCRCLCRRGVCRCLC 16
 34 GVCVCVC---VCVCVC 46
 PRELIMINARY;
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 NCBI_TaxID=9606;
 WCBI_TaxID=7955;
 Q9H654
Q9H654;
 RESULT 37
09465
AC 09465
AC 09465
DT 01-MA
DT 01
 RESULT 38
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 Gaps
 Varva, 999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
Name-CO6Al. 6;
Caenorhabditis elegans.
Enkaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
 3,
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 DB 2; Length 462;
 MCMAINTAY A.A.,
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RELY, 24986; CA430055.1; -.
RESP: 19875; 19876.
RESP: PO2876; 9WGA.
RESP: PO2876; 9WGA.
RINEEPPO: IPRO06039; EGF 11ke.
RESPECT: PS00196; 4FE45 FERREDOXIN; UNKNOWN_1.
RESOSITE; PS00196; 4FE45 FERREDOXIN; UNKNOWN_1.
RESOSITE; PS01208; VWFC_1; 1.
WHYDCHELICAL PROCEST.
** APPORTED TO THE
 "Genome sequence of the nematode C.elegans: A platform for investigating biology.", Science 282:2012-2018(1998).
 Query Match
Best Local Similarity 52.9%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 8; Indels
 2; Indels
Strausberg R., Strausberg R., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) AA472700.1; -. Hypothetical protein.
 NON TER 1 1
SEQUENCE 462 AA; 52504 MW; 9BF8B5754E98355A CRC64;
 al protein. -
152 AA; 15646 MW; 6E254F0BE476D354 CRC64;
 PRT; 1506 AA.
 PRT; 152 AA.
 / Match
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les 9; Conservative 2; Mismatches
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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 67 GGCGCCCRPRCCCCCR 83
 1 GVCRCLCRRGVCRCLC 16
 PRELIMINARY;
 PRELIMINARY;
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Misra S., Crobby M.A., Mungail C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whified E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., Ge Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

MEDLINE=22426069; PubMed=12537572;

"Annotation of the Drosophila melanogaster euchromatic genome: a

Lewis S.E.;

systematic review.";
Genome Biol, 3:RESEARCH0083-RESEARCH0083(2002).

to the EMBL/GenBank/DDBJ databases

Submitted (SEP-2002)

SEQUENCE FROM N.A.

FLYBASE

SEQUENCE FROM N.A.

FLYBASE

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RP SEQUENCE FROM N.A.

RA MEDINE—20196006, PubMed=10731132,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gocage R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Hardon R.C., Rogers Y.H., Blazej R.G., Chamge M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Beson K.Y. Beau A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

RA Beson K.Y. Beau A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

RA Berson K.Y. Beau B. W., Burlor H., Cadiau E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Burlor H., Cadiau E., Bolshakov S.,

RA Burtis R.C., Busam D.A., Burlor H., Cadiau E., Boutove B.,

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RA Boson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Boson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Boloth K.J. Evangelista C.C., Ferraz C., Ferriar S., Fleischmann W.,

RA Goler C., Gabriellan A.E., Gorg I., Wal M.H., IDegwam C.,

A Jolahl M., Kalush P., Karpen G.H., Kez X., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Harnandez J.R., Haorts M.,

RA Harris N.L., Moy W., Murphy B., Wall M.H., IDegwam C.,

A Jalli M., Kalush P., Karpen G.H., Kaz X., Kennison J.A., Melson D.L.,

RA Marson D.R., Moy W., Murphy B., Wall M.H., IDegwam C.,

A Jalli M., Moy W., Murphy B., Wixon K., Musskern D.R., Pacleb J.M.,

Rand B.E., Siden-Kiamos I. S., Honter J., Marson M., Strong R., Sheller E., Spradling A.C., Staphecon M., Strong R., Sheller S., Wall M., Wall M., Strong R., Wall M., Wall
 SEQUENCE FROM N.A.

MEDLINE-22426065; PubMed=12537568;

MEDLINE-22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams R.A., Laverty T., Muzny D.M., Nasison C.R., George R.A., Hoskins R.A., Laverty T., Kichards S., Sodergren E.J., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Whers E.W., Gibbs R.A., Rubin G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Behydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 "The genome sequence of Dross Science 287:2185-2195(2000).
 ORFNames=CG32681;
```

SEQUENCE FROM N.A.
MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:

Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]

genomics perspective."

melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

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 Gaps
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0
 46.4%; Score 52; DB 2; Length 1506; 66.7%; Pred. No. 1.9e+02; ive 0; Mismatches 5; Indels
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AE003450; AAN09260.1; -. Flyases: Fspro052681, CG32681. SEQUENCE 1506 AA; 15995772 CRC64;
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 213
 4 RCLCRRGVCRCLCRR 18
 10; Conservative
 199 RCPSRRGSCSCLKRR
 Best Local Similarity
 Secs
 : 130.5
 Query Match
 Matches
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
 1 GVCRCLCRRGVCRCLCRR 18
 GVCRCLCRRGVCRCLCRR
 g 4
 Adb35047 Theta def
Adb35231 Rhesus th
Ado35242 Rhesus th
Ado35243 Rhesus th
Ado35243 Rhesus th
Ado35249 Anti-vira
Aab3530 Theta def
Abp55297 Anti-vira
Add3526 Anti-vira
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Ado3525 Rhesus th
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Abp5239 Anti-vira
Abp5239 Anti-vira
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 , Search time 115 Seconds
(without alignments)
56.149 Million cell updates/sec
 Description
 2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2002273 seqs, 358729299 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 AAB35030
AAB73286
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 October 26, 2004, 15:13:05
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 US-10-009-317A-33
112
1 GVCRCLCRRGVCRCLCRR 18
 A Geneseq 23Sep04:*
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3: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
 BLOSUM62
Gapop 10.0 , Gapext
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 Length
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Match
 Title:
Perfect score:
Sequence:
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|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|--------------------------|-----------|---------------|----------------|------------------------------------------|--------------|----------------|--------------|---------------|---------------|--------------|--------------------|--------------|---------------------------------------|-----------------|--------------------------------------------------------------------------------------------------|-------------|------------------------------------------------------------------------|
| Aae33864 Enantio-R<br>Aae33802 16% retro<br>Ado32824 Rhesus th<br>Adn08177 Human ret<br>Adn08179 Human ret<br>Adn08178 Human ret<br>Adn08178 Human ret<br>Adn08180 111% retro<br>Aae33806 111% retro<br>Aab3806 Atti-vira<br>Adn08181 Human ret<br>Adn08181 Human ret<br>Adn08181 Rhesus th<br>Ado35230 Rhesus th<br>Ado35249 Rhesus th                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |                          |           |               |                | ; fungus; protozoan;<br>; analogue.      |              |                |              |               |               |              |                    |              | activity against                      |                 | peptides and analogues<br>s used in the treatment of<br>nthic infections, in                     |             | Length 18;<br>Indels 0; Gaps                                           |
| AAE33864 AAE33802 AAE33802 AAE33802 AAO35244 ADMO8177 ADMO8179 ADMO8178 AAE33805 AAE33806 AAE33806 AAE33806 AAE33806 AAE33806 AAE33806 AAE33806 AAE33807 ADO35259 AAE33807 ADO35259 ADO35254                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNMENTS | ); 18 AA.                |           |               | 31.            | oial; cyclic; bacterium;                 |              |                |              | 342.          | 487.          |              | a J, Ouellette AJ; |              | with antimicrobial ozoa and viruses.  | English.        | ta defensin<br>They can be<br>and helmin                                                         |             | .0%; Score 112; DB 4;<br>.0%; Pred. No. 9.2e-06;<br>. 0; Mismatches 0; |
| 799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55<br>799.55 |            | standard; peptide;       |           | (first entry) | in SEQ ID NO:  | ensin; antimicrobi<br>lminth; disinfecta | ن            | Al.            |              | 2000WO-US0128 | , 99US-003094 | CALIFORNIA.  | Tang Y, Yuan       | 1853/04.     | defensin peptide<br>east, fungi, prot | ig 16; 110pp; E | invention provides thei antimicrobial activity. viral, fungal, protozoalts and as food preserval | AA;         | 100.0<br>Similarity 100.0<br>18; Conservative                          |
| 226<br>226<br>332<br>333<br>333<br>333<br>334<br>44<br>44<br>44<br>45<br>44<br>44<br>45<br>44<br>44<br>45<br>46<br>46<br>47<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48<br>48                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            | 1<br>47<br>AB35047       | AAB35047; | 27-MAR-2001   | Theta defensin | Theta defens<br>virus; helmi             | Unidentified | WO200068265-Al | 16-NOV-2000. | 10-MAY-2000;  | 10-MAY-1999;  | (REGC ) UNIV | Selsted ME,        | WPI; 2001-03 | Novel theta<br>bacteria, ye           | Claim 19; Fi    | The present in which have and bacterial, visdisinfectants                                        | Sequence 18 | Query Match<br>Best Local Simi<br>Matches 18;                          |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            | RESULT<br>AAB350<br>ID A | X X       | XE:           | S E            | ¥ <b>2</b>                               | X 8 i        | ₹ <b>%</b> }   | (요)          | \$ E. \$      | { E }         | <b>{</b>     | ZI.                | X K S        | X E E                                 | X S             | <br> <br> <br> <br> <br>                                                                         | SOS         | Que<br>Ber<br>Mat                                                      |

138

Monkey, Rhesus theta defensin, RTD-3; antimicrobial peptide; cyclic, antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.

Rhesus theta defensin peptide, RTD-3.

(first entry)

15-JUL-2004

1. 18 /note= "The peptide is cyclised by a covalent link between these two residues"

Location/Qualifiers

Macaca mulatta.

Key Modified-site

N

GVCRCLCRRGVCRCLCRR 18

ADO35231 standard; peptide; 18

AD03523

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Macaca mulatta.
Synthetic.
 WO200260468-A2.
 13-NOV-2002
 38-AUG-2002.
 ABP53296;
RESULT 2
 ABP53296
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The present invention describes a method (MI) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphace helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS. reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS, reducing the infectivity of a virus; and (c) rendering virus or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is a daministered to a patient who is immunosuppressed or to a subject who is contacting the virus. The present contacting the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is fared to a variance of the anti-viral peptide is sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention
 Anti-viral, viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
 New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
 Tack B;
 Roller R, Mccray PB,
 Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
 Stinski M,
 Disclosure; Page 10; 65pp; English.
 Ŕ
ABP53296 standard; peptide; 18
 39-JAN-2002; 2002WO-US002435.
 30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
 (IOWA) UNIV IOWA RES FOUND.
 (first entry)
 Maury W, Stapleton J,
 WPI; 2002-674815/72.
 Sequence 18 AA;
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30-APR-2003; 2003US-00427715. 30-APR-2002; 2002US-0377071P

22-JAN-2004.

Disulfide-bond US2004014669-A1

Disulfide-bond Disulfide-bond

(REGC ) UNIV CALIFORNIA. Selsted ME, Tran DQ;

```
The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD03527. The theta defeatiled in the claims or appearing as AD035239-AD035257. The theta defeatiled in the claims or appearing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or colution, an inanimate object comprising surface, or a mammal. The solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.
 high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-3
 Example 1; SEQ ID NO 3; 46pp; English.
 WPI; 2004-167945/16.
 Sequence 18 AA;
```

ö

Gaps

ö

100.0%; Score 112; DB 5; Length 18; 100.0%; Pred. No. 9.2e-06; ... ive 0; Mismatches 0; Indels

1 GVCRCLCRRGVCRCLCRR 18

Conservative

Best Local Similarity Matches 18; Conservat

Query Match

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbiscidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from sequence rill, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
ö
 Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
 ö
 Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 ö
 Indels
 ;
 Rhesus theta defensin analogue peptide aRTD-3-NH.
 Mismatches
 Claim 1; SEQ ID NO 16; 46pp; English.
 Location/Qualifiers
 ADO35242 standard; peptide; 18 AA.
 /note= "Amidated"
 ..
0
 18
 GVCRCLCRRGVCRCLCRR 18
 30-APR-2003; 2003US-00427715.
 30-APR-2002; 2002US-0377071P.
 1 GVCRCLCRRGVCRCLCRR
 (first entry)
 18; Conservative
 (REGC) UNIV CALIFORNIA
 3. .16
5. .14
7. .12
 Tran DQ;
 WPI; 2004-167945/16.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
 US2004014669-A1
 Sequence 18 AA
 Macaca mulatta
 Selsted ME,
 15-JUL-2004
 Synthetic
 object.
 Matches
 AD035242
 ò
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the invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism in an environment sate of convert or survival of a microorganism in an environment such as food or survival of a microorganism in an environment such as food or convert or a solution, an inanimate object comprising surface, or a mammal. The solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
 ö
 Monkey; Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 .
100.0%; Score 112; DB 8; Length 18; 100.0%; Pred. No. 9.2e-06; ive 0; Mismatches 0; Indels
 Rhesus theta defensin analogue peptide aRTD-3-OH.
 /note= "Hydroxylated"
 Claim 1; SEQ ID NO 15; 46pp; English.
 Location/Qualifiers
3..16
5..14
 Ä
 ADO35241 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 1 GVCRCLCRRGVCRCLCRR 18
 30-APR-2002; 2002US-0377071P
 30-APR-2003; 2003US-00427715
 (first entry)
 Conservative
 (REGC) UNIV CALIFORNIA
 Tran DQ;
 WPI; 2004-167945/16.
 Best Local Similarity
Matches 18; Conserv
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 US2004014669-A1
 Macaca mulatta,
 Modified-site
 15-JUL-2004
 22-JAN-2004
 Selsted ME,
 Synthetic
 AD035241;
 Query Match
 object.
 RESULT 5
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 Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antihiflammatory, antibacterial, virucide, fungicide, food; contact lens solution, eye wash solution, inflammatory response; microbicidal inhibition, microbistatic growth inhibition, disinfectant, food preservative, bacterial infection, viral infection, disinfectant, fungal infection, haemolytic activity.
 The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD035239-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments.
 or
 Gaps
 Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 .
sequence represents a Rhesus theta defensin analogue peptide.
 Length 18;
 Indels
 Rhesus theta defensin analogue peptide 3:1 aRTD-1-NH.
 100.0%; Score 112; DB 8;
100.0%; Pred. No. 9.2e-06;
ive 0; Mismatches 0;
 Claim 1; SEQ ID NO 17; 46pp; English
 Location/Qualifiers
 Ä.
 /note= "Amidated"
 ADO35243 standard; peptide; 18
 18
 18
 30-APR-2003; 2003US-00427715
 30-APR-2002; 2002US-0377071P
 1 GVCRCLCRRGVCRCLCRR
 1 GVCRCLCRRGVCRCLCRR
 (first entry)
 18; Conservative
 (REGC) UNIV CALIFORNIA
 Tran DO;
 WPI; 2004-167945/16.
 Local Similarity
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 18 AA;
 US2004014669-A1
 Macaca mulatta.
 Modified-site
 15-JUL-2004
 Selsted ME,
 22-JAN-2004
 Synthetic.
 AD035243;
 Query Match
 object.
 Matches
 AD035243
 RESULT
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus a pread within a virally-infected subject (VS), reducing viral burden in a spread within a virally-infected subject (VS), reducing viral burden in a vS, reducing virus shed from a VS, reducing percentage of VS in a VS, (b) reducing the infectivity of a virus, or inducing latency in a VS, (b) reducing the infectivity of a virus, in and (C) rendering virus particles in a population of viruses. (M1) is useful corrections virus particles in a population of viruses. (M1) is useful cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
 Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
 New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The there defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
 Gaps
 ä
 Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.
 Tack
 0
 Score 107; DB 8; Length 18;
Pred. No. 3.2e-05;
 Mccray PB,
 0; Indels
 Roller R,
 100.0%; Prec. ...
 Stinski M,
 Disclosure; Page 10; 65pp; English.
 ABP53298 standard; peptide; 18 AA.
 GVCRCLCRRGVCRCLCR 18
 1 GVCRCLCRRGVCRCLCR 17
 29-JAN-2002; 2002WO-US002435.
 30-JAN-2001; 2001US-0265270P.
 95.5%;
 (IOWA) UNIV IOWA RES FOUND.
 Query Match
Best Local Similarity 100.0
 (first entry)
 Maury W, Stapleton J,
 WPI; 2002-674815/72.
 Sequence 18 AA;
 mulatta.
 WO200260468-A2.
 Homo sapiens
 13-NOV-2002
 08-AUG-2002.
 Macaca mul
Synthetic.
 ABP53298;
 RESULT 7
 ABP53298
 888888
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GFCRCLCRRGVCRCICTR 18

RESULT 9

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administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently infected with the virus. The present sequence represents a chimeric human/rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
 The present invention provides theta defensin peptides and analogues which have annimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
 Gaps
 cyclic; bacterium; fungus; protozoan; food preservative; analogue.
 Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
 ;
0

 .18
/note= "peptide bond cyclises the molecule"

 Query Match 91.1%; Score 102; DB 5; Length 18; Best Local Similarity 83.3%; Pred. No. 0.00011; Matches 15; Conservative 2; Mismatches 1; Indels
 Ouellette AJ;
 Location/Qualifiers
 Claim 4; Page 4; 110pp; English.
 1 GICRCLCRRGVCRCICGR 18
 1 GVCRCLCRRGVCRCLCRR 18
 AAB35030 standard; peptide; 18
 Theta defensin; antimicrobial;
 virus; helminth; disinfectant;
 Yuan J,
 10-MAY-2000; 2000WO-US012842.
 99US-00309487
 Theta defensin SEQ ID NO: 1
 (REGC) UNIV CALIFORNIA
 Tang Y,
 WPI; 2001-031853/04.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 18 AA;
 Sequence 18 AA;
 40200068265-A1
 .0-MAY-1999;
 Unidentified
 27-MAR-2001
 Cross-links
 Selsted ME,
 invention
 AAB35030;
 AAB35030
 8888888888
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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic peptide (I) comprising a theta-defensin peptide in an amphipathic alphabelic structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for inhibiting the growth and conce viral sensets and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject from a viral infection, preventing recurrent viral infection and subject from a viral infection, preventing viral burden in a concern virus shed form a Viral infection status, controlling virus in spead within a virally infected subject (VS). reducing virus shed for a virus in a contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus; and (c) rendering virus so the infectivity of a virus; in sheep, cattle, horses, waine, cate, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject whore the first anti-viral peptide is most preferably administered to a subject who is contacting the virus. The present sequence represents a thesus monkey there defensin anti-viral peptide, which is given in the exemplification of the present invention
 ö
 Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
 New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
 Gaps
 Tack B;
 ;
0
 88.4%; Score 99; DB 5; Length 18; 83.3%; Pred. No. 0.00023; Live 1; Mismatches 2; Indels
 Mccray PB,
 Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
 Roller R,
 Stapleton J, Stinski M,
 Disclosure; Page 10; 65pp; English.
Ą.
 29-JAN-2002; 2002WO-US002435.
 30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
 (IOWA) UNIV IOWA RES FOUND.
 (first entry)
 Query Match
Best Local Similarity 83.3
Matches 15; Conservative
 Sequence 18 AA;
 mulatta.
 WO200260468-A2.
 13-NOV-2002
 08-AUG-2002
 Macaca mul
Synthetic.
 ABP53297;
ABP53297
 Maury W,
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Gaps

88.4%; Score 99; DB 4; Length 18; 83.3%; Pred. No. 0.00023; ive 1; Mismatches 2; Indels

1 GVCRCLCRRGVCRCLCRR 18

Local Similarity 83.3 es 15; Conservative

Best Loca Matches

Query Match

Cyclic defensin fragment

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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy, The present sequence is rheeus monkey theta defensin, RTDI peptide. This sequence is used in the exemplification of the invention
 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
 Gaps
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 ö
 Score 99; DB 6; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
 Hong TB;
 AAE33866 standard; peptide; 18 AA
 Ā
 Example 1; Fig 3C; 72pp; English.
 Cole AM,
 ADD95202 standard; peptide; 18
 18
 18
 GFCRCLCRRGVCRCICTR 18
 18
 83.3%;
 18-APR-2002; 2002WO-US012353
 18-APR-2001; 2001US-0284855P
 1 GVCRCLCRRGVCRCLCRR
GVCRCLCRRGVCRCLCRR
 1 GVCRCICTRGFCRCLCRR
 Macaca mulatta RTD1 peptide
 (first entry)
 (first entry)
 15; Conservative
 (REGC) UNIV CALIFORNIA.
 Waring AJ,
 WPI; 2003-103387/09.
 Local Similarity
 Sequence 18 AA;
 Macaca mulatta
 WO200285401-A1
 29-JAN-2004
 16-APR-2003
 31-OCT-2002
 Lehrer RI,
 AAE33866;
 ADD95202;
 Query Match
 RESULT 11
ADD95202
 Matches
 RESULT 10
 4AE33866
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 BXXXXXX
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This invention describes a novel conjugate for treating prokaryotic confections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote cand intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably a human peptide or protein, especially a phage-holin protein, its active crassitance to penciallin, terracycline, ampiciallin protein, its active conjugate has the structure transport mediator-spacer. The conjugate has the structure transport mediator through a caids and the spacer is poly(glycine and/or lysine), preferably containing 2-6 amino acids and the spacer is linked to the transport mediator through a caids and the spacer is linked to the transport mediator through a cide apply glycine and/or lysine), preferably containing 2-6 amino acids and the spacer is linked to the transport mediator through a cide and the invention have antibacterial activity and are used, crespecially in combination with antibiotics, for treating prokaryotic, specially bacterial, infections, especially where the pathogen is products of the invention have antibiotics and then the PNA is directed against the antibiotic resistance gene where the PNA is directed against containing the condministered antibiotic and then the PNA is directed against antibiotic resistance gene the conjugate will render the bacteria cused sensitive to co-administered antibiotics i.e. 'old' antibiotics can be congenicate accessfully the especial defensin fragment described in the conception.
 ö
 New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
 bacterial infection, human pathogen, holin, defensin,
peptide nucleic acid, PNA, penicillin, tetracycline, ampicillin,
kanamycin, antibiotic, antibacterial, antibiotic-resistance gene, cyclic.

 .18
/note= "Residue 1 and residue 18 bond to form a cyclic

 Gaps
 ö
 Score 99; DB 7; Length 18; Pred. No. 0.00023; 1; Mismatches 2; Indels
 Waldeck W;
 Braun K, Braun I, Debus J, Pipkorn R,
 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 Location/Qualifiers
 Disclosure; Fig 10; 34pp; German
 18
 8
 18-JAN-2002; 2002DE-01001862.
 88.4%;
 17-JAN-2003; 2003WO-DE000124
 GVCRCLCRRGVCRCLCRR
 Query Match
Best Local Similarity 83.3
Matches 15; Conservative
 moiety"
3. .16
5. .14
7. .12
 WPI; 2003-689464/65.
 Misc-difference
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 WO2003059392-A2
 Sequence 18 AA;
 Unidentified
 24-JUL-2003.
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RESULT 12

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Gerdes

ADD35357 ID ADD3 XX

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for preparing a composition for treatment and/or prevention of bactersamia for binding bacterial products such as lipopolysaccharide bactersamia for binding bacterial products such as lipopolysaccharide of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding), immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so provides a better and simpler treatment.
 This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
 Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
 Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide; cyclic; antimicrobial, antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fungal infection; haemolytic activity.
 microbial cell-wall biosynthesis; immunomodulation; anticoagulant
 Score 99; DB 8; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
 Brunner N,
 Rhesus theta defensin peptide, RTD-1.
 Labischinski H,
 Example 1; SEQ ID NO 1; 28pp; German.
 Location/Qualifiers
 ADO35229 standard; peptide; 18 AA
 18
 18
 Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
 30-MAY-2003; 2003WO-EP005694
 13-JUN-2002; 2002DE-01026216
 1 GVCRCLCRRGVCRCLCRR
 (first entry)
 (FARB) BAYER HEALTHCARE
 Newton B,
 WPI; 2004-071500/07
 WO2003105883-A1
 Sequence 18 AA;
 Key
Modified-site
 15-JUL-2004
 AD035229;
 Ladel C,
 RESULT 14
 %XCCCCCCCCCCCCX%X444X6X1X6X6X6X6X6X6X6X8X8X8X8
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 The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraocular pressure, such as prostaglandin and the antimicrobial peptide work spresgistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, coular cell dysplasia, irritation and inflammation of conjunctiva, hyperplementation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
 rhesus theta defensin-1, RTD-1; bacteraemia; lipopolysaccharide; LPS;
lipteichonic acid; LTA; septic shock; antibacterial; fungicide; virucide;
immunomodulator; anticoagulant activity;
 antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypetrension; hypersemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
 Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial peptide.
 Gaps
 ;
0
 Score 99; DB 8; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
 Rhesus theta-defensin-1 (RTD-1) peptide.
 Antimicrobial peptide theta-defensin.
 Disclosure; Page 11; 11pp; English.
 Ş
 Ą.
 ADD35357 standard; peptide; 18
 18
 ADG70012 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 88.4%;
Local Similarity 83.3%;
les 15; Conservative 1
 21-MAR-2003; 2003WO-US008935.
 21-MAR-2002; 2002US-0367071P.
 GFCRCLCRRGVCRCICTR
 (first entry)
 (first entry)
 (CAYM-) CAYMAN CHEM CO
 Johnson J;
 WPI; 2004-011506/01
 WO2003079997-A2
 Sequence 18 AA;
 15-JAN-2004
 02-OCT-2003.
 11-MAR-2004
 ADD35357;
 Maxey KM,
 ADG70012;
 Query Match
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RESULT 13

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Gaps

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or south or survival of a microorganism in an environment such as food or south or survival of a microorganism in an environment such as food or solution, an inanimate object compatigned surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from acterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
 Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial, virucide, fungicide, food, contact lans solution; eye wash solution, inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant, food preservative, bacterial infection, viral infection; disinfectant, fungal infection; haemolytic activity.
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Score 99; DB 8; Length 18;
Pred. No. 0.00023;
1; Mismatches 2; Indels
 Rhesus theta defensin analogue peptide aRTD-1-NH.
 Example 2; SEQ ID NO 12; 46pp; English
 /note= "Hydroxylated"
Location/Qualifiers
 ADO35239 standard; peptide; 18 AA
 18
 138
 30-APR-2003; 2003US-00427715
 30-APR-2002; 2002US-0377071P
 Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
 GFCRCLCRRGVCRCICTR
 1 GVCRCLCRRGVCRCLCRR
 15-JUL-2004 (first entry)
 (REGC) UNIV CALIFORNIA.
 Selsted ME, Tran DQ
 WPI; 2004-167945/16.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 US2004014669-A1
 Sequence 18 AA;
 Modified-site
 22-JAN-2004.
 AD035239;
 object.
 RESULT 16
 AD035239
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 q
 The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO3523-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for wheamolytic activity. The present sigh antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
 ö
 Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 ö
 88.4%; Score 99; DB 8; Length 18; 83.3%; Pred. No. 0.00023; ive 1; Mismatches 2; Indels
 Rhesus theta defensin analogue peptide aRTD-1-OH.
 Example 1; SEQ ID NO 1; 46pp; English.
 ADO35238 standard; peptide; 18 AA.
 1 GVCRCLCRRGVCRCLCRR 18
 30-APR-2003; 2003US-00427715
 30-APR-2002; 2002US-0377071P
 1 GFCRCLCRRGVCRCICTR
 (first entry)
 15; Conservative
 (REGC) UNIV CALIFORNIA.
 Selsted ME, Tran DQ;
 WPI; 2004-167945/16.
 Local Similarity
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 18 AA;
 US2004014669-A1
 22-JAN-2004
 15-JUL-2004
```

object.

Query Match

Matches

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AD035238

RESULT 15 AD035238

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Gaps ö

Macaca mulatta,

Synthetic.

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food preservative; bacterial infection; viral infection; fungal infection; haemolytic activity; cyclic.
 Tran DQ;
 WPI; 2004-167945/16.
 US2004014669-A1
 Sequence 18 AA;
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Macaca mulatta
 Modified-site
 22-JAN-2004.
 Selsted ME,
 15-JUL-2004
 Synthetic
 AD035263;
 object
 셤
 CXXXXXXXXX
 ठे
 The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or or obtained, a solution (e.g., contact lens solution, or eye wash solution, an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The there defensing have becterial, viral, fungal or other infection. The there defensing have high antimicrobial activity and low haemolytic activity. The present
 ;
0
 Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial, antilifiammatory; antibacterial; virucide; fungicide; food, contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant;
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 ö
 sequence represents a Rhesus theta defensin analogue peptide
 88.4%; Score 99; DB 8; Length 18; 83.3%; Pred. No. 0.00023; tive 1; Mismatches 2; Indels
 Rhesus theta defensin analogue peptide RTD-5.
 Claim 1; SEQ ID NO 13; 46pp; English
 Location/Qualifiers
 Ą.
 /note= "Amidated"
 ADO35256 standard; peptide; 18
 18
 18
 30-APR-2003; 2003US-00427715.
 30-APR-2002; 2002US-0377071P.
 1 GVCRCLCRRGVCRCLCRR
 1 GFCRCLCRRGVCRCICTR
 (first entry)
 Local Similarity 83.3
les 15; Conservative
 (REGC) UNIV CALIFORNIA
 3. .16
5. .14
7. .12
 Tran DQ;
 WPI; 2004-167945/16.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
 US2004014669-A1
 Sequence 18 AA;
 Macaca mulatta
 15-JUL-2004
 Selsted ME,
 22-JAN-2004
 Synthetic
 AD035256;
 Query Match
 object.
 Matches
 RESULT 17
 AD035256
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 AXXXXXXXXXXXX
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbisical inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
 ò
 Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 /note= "The peptide is cyclised by a covalent link between these two residues"
 .
0
 Query Match 88.4%; Score 99; DB 8; Length 18; Best Local Similarity 87.5%; Pred. No. 0.00023; Matches 14; Conservative 2; Mismatches 0; Indels
 Monkey RTD-1 (rhesus theta defensin 1) 2X protein.
 Claim 1; SEQ ID NO 30; 46pp; English.
Location/Qualifiers
 ADO35263 standard; protein; 38 AA.
 30-APR-2003; 2003US-00427715.
 30-APR-2002; 2002US-0377071P.
 1 GICRCLCRRGVCRCIC 16
 1 GVCRCLCRRGVCRCLC 16
 (first entry)
 1. .18
/note= '
 (REGC) UNIV CALIFORNIA
 3. .16
5. .14
7. .12
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AAB35037 standard; peptide; 18

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The there detailed in the claims or appearing as ADO35239-ADO35257. The there defensin analogue is useful for reducing growth or survival of a microorganism and is useful for reducing or inhibiting crowth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbicidal inhibition of survival of microorganism as well as microbicates are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present sequence is protein containing 2 copies of the rhesus monkey theta or Monkey, Rhesus theta defensin, RTD-1, antimicrobial peptide, antimicrobial, antinflammatory, antibacterial, virucide, fungicide; food; contact lens solution; eye wash solution; inflammatory response, microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate .2
 /note= "CNBr cleavage site" 20. .21 /note= "CNBr cleavage site" cocation/Qualifiers Example 4; Fig 17a; 46pp; English. "RTD-1" 21. .38 /note= "RTD-1" 30-APR-2003; 2003US-00427715 30-APR-2002; 2002US-0377071P (REGC ) UNIV CALIFORNIA. 2. .19 /note= Tran DQ; WPI; 2004-167945/16. N-PSDB; ADO35262. JS2004014669-A1 Sequence 38 AA; Macaca mulatta. Synthetic. Key Cleavage-site Cleavage-site Selsted ME, 22-JAN-2004 Peptide Peptide

RESULT 20

ABP53294

ö Gaps ; Score 99; DB 8; Length 38; Pred. No. 0.00041; 1; Mismatches 2; Indels 88.4%; Local Similarity 83.3 les 15, Conservative Query Match Best Loca Matches

13 1 GVCRCLCRRGVCRCLCRR 18 GFCRCLCRGVCRCICTR

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RESULT 19 AAB35037

The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives Gaps Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue. Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses. ; Length 18; / Match 84.8%; Score 95; DB 4; Length 18; Local Similarity 87.5%; Pred. No. 0.00062; les 14; Conservative 1; Mismatches 1; Indels Rhesus macaque theta defensin peptide SEQ ID NO: 8. Ouellette AJ Example 1; Fig 2; 110pp; English Selsted ME, Tang Y, Yuan J, 10-MAY-2000; 2000WO-US012842 99US-00309487 1 GVCRCLCRRGVCRCLC 16 (first entry) (REGC ) UNIV CALIFORNIA WPI; 2001-031853/04 Sequence 18 AA; Rhesus macaque. WO200068265-A1 10-MAY-1999; 27-MAR-2001 16-NOV-2000 AAB35037; Query Match Matches 용 ઠ

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Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor; viral proliferation inhibitor. Synthetic anti-viral human theta defensin peptide HTD-1 SEQ ID NO:27 ABP53294 standard; peptide; 18 AA. 29-JAN-2002; 2002WO-US002435 30-JAN-2001; 2001US-0265270P 01-AUG-2001; 2001US-0309368P (first entry) WO200260468-A2 13-NOV-2002 Homo sapiens 08-AUG-2002 Synthetic. ABP53294; 

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WPI; 2003-103387/09.
 18
Misc-difference 18
 Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Misc-difference
 Misc-difference
 Disulfide-bond
 WO200285401-A1
 Unidentified
 16-APR-2003
 Sequence 18
 AAE33863;
 Query Match
 Best Loc
Matches
 RESULT 22
 AAE33863
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 g
 The present invention describes a method (MI) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabatical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of antiparticle fargarden. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or reating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus in special shed from a VS, reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS, (b) reducing virus latentivity of a virus; and (c) reducing latency in a voi, (b) reducing the infectivity of a virus in sheep, cattle, horses, swine, contaminated tissue or fluid sample safe for use, or reducing the number of infections virus particles in a population of viruses (MI) is useful cars, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered to a patient who are subject who is anti-viral peptide is a chuman intera defensin anti-viral peptide is a human there defensin anti-viral peptide, which is caused.
 ö
 Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial; human; cyclic.
 /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. 16
7. 12
 comprising a Theta-
 Gaps
 Tack
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 PB,
 82.1%; Score 92; DB 5; Length 18; 66.7%; Pred. No. 0.0013; ive 4; Mismatches 2; Indels
 Mccray
 given in the exemplification of the present invention
 New method of using a first anti-viral peptide compi
defensin peptide in an amphipathic Alpha-helical sti
environment for reducing the infectivity of a virus
 Roller R,
 Location/Qualifiers
 Stinski M,
 AA.
 Disclosure; Page 9; 65pp; English
 AAE33801 standard, peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 (IOWA) UNIV IOWA RES FOUND.
 (first entry)
 Human retrocyclin peptide.
 12; Conservative
 Stapleton J,
 WPI; 2002-674815/72
 Best Local Similarity
Matches 12; Conserv
 Misc-difference
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 18 AA;
 Homo sapiens
 16-APR-2003
 AAE33801;
 Maury W,
 Query Match
 RESULT 2
 à
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The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide
 Retrocyclin, infection; sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 "Linked to amino acid at position 18 to form a structure"
 Gaps
 /note= "Linked to amino acid at position 1 to form a cyclic structure"
/note= "Linked to amino acid at position 1 to form a cyclic structure"
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 ö
 Score 92; DB 6; Length 18; Pred. No. 0.0013; 4; Mismatches 2; Indels
 Hong TB;
 1. .18
/note= "D-form residues"
 Enantio-retrocyclin peptide analogue
 Location/Qualifiers
 Ā
 Cole AM,
 Claim 9; Page 24; 72pp; English
 4
 18
 18
 AAE33863 standard; peptide; 18
 82.1%;
66.7%;
 18-APR-2001; 2001US-0284855P
 18-APR-2002; 2002WO-US012353
 1 GICRCICGRGICRCICGR
 1 GVCRCLCRRGVCRCLCRR
 (first entry)
 Local Similarity
nes 12; Conservative
 (REGC) UNIV CALIFORNIA
 cyclic 33. 165. 145. 17
 'note=
 Lehrer RI, Waring AJ,
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Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
 REGC) UNIV CALIFORNIA.
[LEHR/) LEHRER R I.
[WARI/) WARING A J.
 REGC) UNIV CALIFORNIA
 cehrer RI, Waring AJ,
 WPI; 2003-103387/09
 Sequence 18 AA;
 402004033479-A2
 WO200285401-A1
 15-JUL-2004
 22-APR-2004.
 Lehrer RI,
 ADN08176
 (HONG/)
 COLE/)
 RESULT 23
ADN08176
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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular corpulation of administering an effective dose of retrocyclin to the corpulation of againsm by administering an effective dose of retrocyclin to the microbial organisms; a method for administering arestrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and viral infection such as HIV-1. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful and viral infections. This sequence represents a retrocyclin cuch and viral infections. This sequence represents a retrocyclin cuch as the invention.
 d retrocyclin peptides and cyclic polypeptides, useful as and prophylactic agents for treating and preventing microbial
 Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
 Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32
 ;
 Score 92; DB 8; Length 18;
Pred. No. 0.0013;
4; Mismatches 2; Indels
 Mccray
 Roller R,
 Claim 9; SEQ ID NO 1; 82pp; English
 Stinski M,
 ABP53299 standard; peptide; 18 AA
 18
 82.1%;
 30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
 29-JAN-2002; 2002WO-US002435
 1 GVCRCLCRRGVCRCLCRR
 GICRCICGRGICRCICGR
 (first entry)
 Local Similarity 66.7
nes 12; Conservative
 Maury W, Stapleton J,
 (IOWA) UNIV IOWA RES
 therapeutic and propl
and viral infections
 WPI; 2004-340883/31.
 NPI; 2002-674815/72
 N-PSDB; ADNO8193
 Sequence 18 AA;
 mulatta
 WO200260468-A2
 13-NOV-2002
 Homo sapiens
 08-AUG-2002
 Macaca mul
Synthetic.
 ABP53299;
 Query Match
 RESULT 24
 ABP53299
 8
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiancy virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful for modelling and screening novel sequence is human retrocyclin peptide analogue
 retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.
 Gaps
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 ..
0
 Score 92; DB 6; Length 18;
Pred. No. 0.0013;
1; Mismatches 2; Indels
 Hong
 Disclosure, Page 24; 72pp; English.
 Æ
 Human retrocyclin peptide, RC-100.
 Cole AM,
 4.
 ADN08176 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 |:|||:|||||
1 GICRCICGRGICRCICGR 18
 18-APR-2002; 2002WO-US012353
 18-APR-2001; 2001US-0284855P
 06-MAY-2003; 2003WO-US014106
 06-MAY-2002; 2002US-00141645
 (first entry)
 LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
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New method of using a first anti-viral peptide comprising a Theta-

Cole AM,

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Gaps

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18-APR-2002; 2002WO-US012353
 Best Loca
Matches
 RESULT 26
 8
 원
 The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphace belical structure in a lipid environment for reducing the infectivity of a virus. (I) can have viruncide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in subject harbouring a latent virus, controlling virus shed from a VS. reducing percentage of VS in a viru a virally-infected subject (VS), reducing virus latent virus of virus of virus butten in a viruly in a viruly percentage of VS in a virul infections virus principle safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus; in sheep, cattle, horses, waine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is immunosuppressed or to a subject who is chronically, latently or acutely infected with the virus. The present sequence represents a chimeric human/rheaus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
 ö
 Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 /note= "Linked to amino acid at position 18 to form a cyclic structure"
3. .16
5. .14
defensin peptide in an amphipathic Alpha-helical structure in a lipid
environment for reducing the infectivity of a virus.
 Gaps
 /note= "Linked to amino acid at position 1 to form a
 ;
 Score 89; DB 5; Length 18;
Pred. No. 0.0028;
3; Mismatches 3; Indels
 Location/Qualifiers
 Disclosure; Page 10; 65pp; English
 Ą.
 I15Y retrocyclin peptide analogue.
 cyclic structure'
 ë.
 18
 AAE33804 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 79.5%;
 (first entry)
 Query Match 79.5
Best Local Similarity 66.7
Matches 12; Conservative
 . .12
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Key
Misc-difference
 Sequence 18. AA;
 WO200285401-A1
 Unidentified
 16-APR-2003
 31-OCT-2002
 AAE33804;
 25
 RESULT 25
AAE33804
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 /note= "Linked to amino acid at position 18 to form a cyclic structure"
5. .14
7. .12
 Gaps
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections of treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 .
0
 /note= "Linked to amino acid at position 1 to cyclic structure"
 / Match 79.5%; Score 89; DB 6; Length 18; Local Similarity 66.7%; Pred. No. 0.0028; les 12; Conservative 3; Mismatches 3; Indels
 Enantio-RC-101 retrocyclin peptide analogue.
 Hong TB;
 1. .18
'note= "D-form residues"
 Location/Qualifiers
 Ą
 Cole AM,
 Claim 9; Page 24; 72pp; English.
 AAE33864 standard; peptide; 18
 18
 18
 18-APR-2002; 2002WO-US012353
18-APR-2001; 2001US-0284855P
 1 GVCRCLCRRGVCRCLCRR
 (first entry)
 (REGC) UNIV CALIFORNIA
 Waring AJ,
 WPI; 2003-103387/09
 Misc-difference
 Disulfide-bond
Disulfide-bond
Misc-difference
 Misc-difference
 Sequence 18 AA;
 Disulfide-bond
 WO200285401-A1
 Unidentified
 16-APR-2003
 Lehrer RI,
 AAE33864;
 Query Match
```

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1 GVCRCLCRRGVCRCLCRR
 (first entry)
 Local Similarity 66.7
les 12; Conservative
 cyclic 83.165.14
 /note=
 (REGC) UNIV CALIFORNIA
 Waring AJ,
 WPI; 2003-103387/09
 WPI; 2003-103387/09
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Key
Misc-difference
 Sequence 18 AA;
 WO200285401-A1
 Unidentified
 31-OCT-2002.
 16-APR-2003
 Lehrer RI,
 AAE33802;
 Query Match
 Matches
 AAE33802
 RESULT
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually retracked diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 ಹ
 Gaps
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 /note= "Linked to amino acid at position 18 to form cyclic structure"
3. .16
5. .14
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
 /note= "Linked to amino acid at position 1 to form cyclic structure"
 ö
 Score 89; DB 6; Length Lo, Pred. No. 0.0028;
 Hong TB;
 Hong TB;
 Location/Qualifiers
 Disclosure; Page 24; 72pp; English.
 ġ.
 Waring AJ, Cole AM,
 16Y retrocyclin peptide analogue.
 Cole AM,
 transmitted diseases, vaginosis.
 18
 18
 79.5%;
61.1%;
 18-APR-2001; 2001US-0284855P
 18-APR-2002; 2002WO-US012353
 18-APR-2001; 2001US-0284855P
 |:|||:| :|:|||:| | GICRCICGR
 AAE33803 standard; peptide;
 1 GVCRCLCRRGVCRCLCRR
 Query Match
Best Local Similarity 61.12
Best Local 11; Conservative
 (first entry)
 (REGC) UNIV CALIFORNIA
 (REGC) UNIV CALIFORNIA
 Waring AJ,
 WPI; 2003-103387/09
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Misc-difference
 Sequence 18 AA;
 WO200285401-A1
 Unidentified
 16-APR-2003
 31-OCT-2002
 Lehrer RI,
 Lehrer RI,
 AAE33803;
 AAE33803
 RESULT
 NAME OF A STATE OF OF THE STATE #X4X1X4X44144X8XX00000000XX8
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 Gaps
New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
 /note= "Linked to amino acid at position 18 to form cyclic structure"
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or
 ;
0
 "Linked to amino acid at position 1 structure"
 Length 18;
 79.5%; Score 89; DB 6; Length 18;
66.7%; Pred. No. 0.0028;
ive 3; Mismatches 3; Indels
 ŢB;
 Location/Qualifiers
 Ź
 R9K retrocyclin peptide analogue.
 Cole AM,
 transmitted diseases, vaginosis.
 Claim 9; Page 24; 72pp; English.
 AAE33802 standard; peptide; 18
 18
 18
 18-APR-2001; 2001US-0284855P
 18-APR-2002; 2002WO-US012353
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 Monkey, Rhesus theta defensin, RTD, antimicrobial peptide, antimicrobial, antiinflammatory; antibacterial; virucide, fungicide, food, contact lens solution; eye wash solution, inflammatory response; microbicidal inhibition, microbistatic growth inhibition, disinfectant; food preservative, bacterial infection; viral infection; disinfectant fungal infection;
 ö
 The invention relates to a theta defensin analogue defined by formulae
 Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Gaps
 ;
 treating patients having the infections, such as HIV, sexually
 Score 89; DB 6; Length 18;
Pred. No. 0.0028;
5; Mismatches 2; Indels
 Rhesus theta defensin analogue peptide 5:3 aRTD-3-NH.
 Claim 1; SEQ ID NO 18; 46pp; English.
 Location/Qualifiers 6. .15 8. .13
 ¥.
 transmitted diseases, vaginosis.
 Claim 9; Page 24; 72pp; English.
 'n
 |:|||:| :|:|||:| | GICRCICGR 18
 ADO35244 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 30-APR-2002; 2002US-0377071P.
 30-APR-2003; 2003US-00427715.
 Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
 (first entry)
 (REGC) UNIV CALIFORNIA.
 WPI; 2004-167945/16.
 Disulfide-bond
Disulfide-bond
Modified-site
 US2004014669-A1.
 Sequence 18 AA;
 mulatta.
 15-JUL-2004
 22-JAN-2004
 Selsted ME,
 Macaca mul
Synthetic.
 ADO35244;
 AD035244
CXSXLXBXBXBXBXBXBXBXBXBXBXBXXBXAAABBXSCXXXXBXBXBXAXBX
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defensin analogue is useful for reducing or inhibiting growth or survival of an incroorganism in an environment capable of sustaining the growth or survival or survival of the microorganism and is useful for reducing or inhibiting growth or survival of the microorganism and is useful for reducing or inhibiting or counterful or survival of a microorganism in an environment such as food or food product, a solution (e.g., conteat lens solution), or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
 New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
 retrocyclin, cyclic, primate, retroviral infection;
circular minidefensin, antibacterial, virucide, vaccine, immunotherapy;
 The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated mucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to the cell; a method for killing microbial
 ;
 Query Match 79.5%; Score 89; DB 8; Length 18; Best Local Similarity 88.2%; Pred. No. 0.0028; Matches 15; Conservative 0; Mismatches 2; Indels
 Claim 9; SEQ ID NO 2; 82pp; English.
 Human retrocyclin peptide, RC-101.
 Ź
 Cole AM,
 ADN08177 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCR 17
 06-MAY-2003; 2003WO-US014106
 06-MAY-2002; 2002US-00141645
 GVARCLCRRGVCRCLAR
 microbial; viral; human.
 UNIV CALIFORNIA
 Waring AJ,
 LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
 WPI; 2004-340883/31.
 WO2004033479-A2.
 Sequence 18 AA;
 Homo sapiens.
 15-JUL-2004
 22-APR-2004
 RI,
 Synthetic.
 ADN08177;
 (REGC)
 (COLE/)
 (WARI/)
 Lehrer
 LEHR/)
 RESULT 30
 88999999999999888
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organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides as a vaccine as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
 New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
 The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primare retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to the cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin to the microbial organisms; a method for administering restrocyclin to the therapeutic agent to a patient with an established microbial or viral
 retrocyclin, cyclic, primate, retroviral infection,
circular minidefensin, antibacterial, virucide, vaccine, immunotherapy,
 Gaps
 ö
 Score 89; DB 8; Lengtn 10, Pred. No. 0.0028;
 Hong TB;
 Claim 9; SEQ ID NO 4; 82pp; English.
 ADN08179 standard; peptide; 18 AA.
 Human retrocyclin peptide, RC-103
 Cole AM,
 138
 18
 79.5%;
 06-MAY-2002; 2002US-00141645.
 06-MAY-2003; 2003WO-US014106
 1 GICRCICGKGICRCICGR
 1 GVCRCLCRRGVCRCLCRR
 Ouery Match
Best Local Similarity 61.1.
Local Similarity 61.1.
Conservative
 (first entry)
 peptide of the invention
 microbial; viral; human.
 (REGC) UNIV CALIFORNIA.
(LEHR/) LEHRER R I.
(WARI/) WARING A J.
 Lehrer RI, Waring AJ,
 LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
 WPI; 2004-340883/31.
 WO2004033479-A2.
 Sequence 18 AA;
 Homo sapiens.
Synthetic.
 15-JUL-2004
 22-APR-2004.
 ADN08179;
 (COLE/)
 RESULT 31
 ADN08179
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 88888888888888888
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0
infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin
 trocyclin peptides and cyclic polypeptides, useful as prophylactic agents for treating and preventing microbial
 The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to the cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin to the microbial organisms; a method for administering restrocyclin as a therapeutic agent to a patient with an established microbial or viral infection, and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and
 retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
 Gaps
 ..
0
 79.5%; Score 89; DB 8; Length 18; 66.7%; Pred. No. 0.0028; ive 3; Mismatches 3; Indels
 3; Mismatches
 TB;
 Claim 9; SEQ ID NO 3; 82pp; English.
 ADN08178 standard; peptide; 18 AA
 Human retrocyclin peptide, RC-102
 Cole AM,
 18
 18
 06-MAY-2002; 2002US-00141645
 06-MAY-2003; 2003WO-US014106
 1 GVCRCLCRRGVCRCLCRR
 GICRCICGRGICRCYCGR
 (first entry)
 UNIV CALIFORNIA.
LEHRER R I.
WARING A J.
COLE A M.
 peptide of the invention.
 New isolated retrocyclin
 12; Conservative
 microbial; viral; human.
 RI, Waring AJ,
 and viral infections.
 WPI; 2004-340883/31.
 Best Local Similarity
 WO2004033479-A2.
 therapeutic and
 Sequence 18 AA;
 Homo sapiens.
 22-APR-2004.
 15-JUL-2004
 Synthetic.
 ADN08178;
 Query Match
 (REGC) (
(LEHR/) I
(WARI/) ;
 (COLE/)
 Lehrer
 Matches
 RESULT 32
 ADN08178
 88888888888888
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us-10-009-317a-33.rag

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sequence is human retrocyclin peptide analogue
 Sequence 18 AA;
 Query Match
 RESULT 34
 Matches
 SXS
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present
virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
 Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 ๙
 Gaps
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 /note= "Linked to amino acid at position 1 to form cyclic structure"
 /note= "Linked to amino acid at position 18 to cyclic structure"
3. .16
5. .14
7. .12
 ô
 79.5%; Score 89; DB 8; Length 18; 66.7%; Pred. No. 0.0028; ive 3; Mismatches 3; Indels
 Hong TB;
 Location/Qualifiers
 AAE33805 standard; peptide; 18 AA.
 12Y retrocyclin peptide analogue.
 Cole AM,
 Claim 9; Page 24; 72pp; English
 18
 18
 18-APR-2002; 2002WO-US012353
 18-APR-2001; 2001US-0284855P
 1 GVCRCLCRRGVCRCLCRR
 GICRCYCGRGICRCICGR
 (first entry)
 Query Match 79.5
Best Local Similarity 66.7
Matches 12; Conservative
 (REGC) UNIV CALIFORNIA
 Lehrer RI, Waring AJ,
 WPI; 2003-103387/09.
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Key
Misc-difference
 Sequence 18 AA
 WO200285401-A1
 Jnidentified
 16-APR-2003
 AAE33805;
 RESULT 33
 8888888888
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 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HTV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 Retrocyclin, infection, sexually transmitted disease, gene therapy, HIV, human immunodeficiency virus, bacterial vaginosis, ophthalmic infection, antibiotic modelling, antimicrobial, cyclic.
 "Linked to amino acid at position 18 to form a structure"
 Gaps
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 ö
 amino acid at position 1 to
Score 88; DB 6; Length 18;
Pred. No. 0.0035;
3; Mismatches 3; Indels
 3; Mismatches
 TB;
 Hong
 Location/Qualifiers
 Ā
 IllY retrocyclin peptide analogue.
 /note= "Linked to cyclic structure"
 Cole AM,
 Claim 9; Page 24; 72pp; English.
 1 GVCRCLCRRGVCRCLCRR 18
 18
 AAE33806 standard; peptide; 18
 18-APR-2002; 2002WO-US012353.
 18-APR-2001; 2001US-0284855P.
Match 78.6%;
Local Similarity 66.7%;
hes 12; Conservative
 1 GYCKCICGRGICRCICGR
 (first entry)
 /note= 7
cyclic E
3.16
5..14
 (REGC) UNIV CALIFORNIA
 Lehrer RI, Waring AJ,
 WPI; 2003-103387/09.
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Key
Misc-difference
 AA;
 WO200285401-A1.
 Unidentified
 16-APR-2003
 Sequence 18
 31-OCT-2002
 AAE33806;
 Query Match
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Length

DB 6;

78.6%; Score 88;

us-10-009-317a-33.rag

1 GVCRCLCRRGVCRCLCRR 18

Page 18

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 The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide, an isolated nucleic acid encoding a primate restrocyclin, a method for preventing retroviral infection in a cell by administering an effective dose of a circular corganisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering restrocyclin as a microbial organism; and a method for administering restrocyclin as a correction, and a method for administering restrocyclin as a correction, and a method for administering restrocyclin as a prophylactic agent to prevent a microbial or viral infection, and a method for administering restrocyclin as a prophylactic developing such infection. The retrocyclin peptide has antibacterial and viral infection such as HIV-1. The retrocyclin peptide can be used to risat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as the respective and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
 ö
 New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
 retrocyclin; cyclic; primate; retroviral infection; circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
 Gaps
 Gaps
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0
 ö
 Query Match 78.6%; Score 88; DB 8; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0035; Matches 12; Conservative 3; Mismatches 3; Indels
Fred. No. 0.0035;
 Hong TB;
 Claim 9; SEQ ID NO 5; 82pp; English.
 Human retrocyclin peptide, RC-104.
 AA.
 Cole AM,
 66.7%; Pre-
 1 GICRCICGRGYCRCICGR 18
 ADN08180 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 06-MAY-2003; 2003WO-US014106
 06-MAY-2002; 2002US-00141645.
 (first entry)
 12; Conservative
 microbial; viral; human.
 (REGC) UNIV CALIFORNIA.
 Waring AJ,
 LEHRER R I.
WARING A J.
COLE A M.
HONG T B.
 WPI; 2004-340883/31.
 Best Local Similarity
 WO2004033479-A2.
 Sequence 18 AA;
 Homo sapiens.
 15-JUL-2004
 22-APR-2004.
 Cehrer RI,
 Synthetic.
 ADN08180;
 (COLE/) (HONG/) H
 WARI/)
 Matches
 RESULT 35
 ADN08180
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The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide, an isolated nucleic caid encoding a primate retrocyclin, a method for preventing retroviral infection in a cell by administering an effective dose of a circular corganisms by administering an effective dose of retrocyclin to the cell; a method for killing microbial organisms, a method for administering restrocyclin to the microbial organisms, a method for administering restrocyclin as a charapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient a risk of developing such infection. The retrocyclin peptide has antibacterial and viruide activities. The retrocyclin peptide can be used as a vaccine infection such as HIV-1. The retrocyclin peptide can be used as a vaccine can can be used in immunotherapy. The peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
 New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
 retrocyclin; cyclic; primate; retroviral infection;
circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
 ö
 78.6%; Score 88; DB 8; Length 18; 66.7%; Pred. No. 0.0035; ive 3; Mismatches 3; Indels
 Cole AM, Hong TB;
 Claim 9; SEQ ID NO 6; 82pp; English.
 ADN08181 standard; peptide; 18 AA.
 Human retrocyclin peptide, RC-105.
 1 GVCRCLCRRGVCRCLCRR 18
 06-MAY-2003; 2003WO-US014106
 06-MAY-2002; 2002US-00141645
 (first entry)
 12; Conservative
 microbial; viral; human.
 (REGC) UNIV CALIFORNIA.
 Lehrer RI, Waring AJ,
 (LEHR/) LEHRER R I.
(WARI/) WARING A J.
(COLE/) COLE A M.
(HONG/) HONG T B.
 WPI; 2004-340883/31.
 Query Match
Best Local Similarity
Matches 12; Conserv
 WO2004033479-A2
 Sequence 18 AA;
 sapiens.
 15-JUL-2004
 22-APR-2004.
 Synthetic
 ADN08181;
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29-JAN-2002; 2002WO-US002435.

RESULT 37 AAB35046

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The present invention describes a method (M1) of using a first anti-viral comprising a theta-defensin peptide in an amphipathic alphace peptide (I) comprising a theta-defensin peptide in an amphipathic alphace helical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used for include virus and so can be used for inhibiting the growth and confideration of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject from a viral infection, preventing recurrent viral infection in a subject from a virally-infection, preventing virus shed from a VS, reducing virus latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus latency in a VS, reducing virus shed from a VS, reducing virus and (C) reducing virus shed from a VS, reducing virus infections virus shed from a VS, reducing virus and (C) reducing virus of virus and (C) reducing virus of virus and (C) reducing virus shed from a population of viruses. (M1) is useful to retain and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is a diministered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is mannistered to a patient whose is immunosuppressed or to a subject who is contacting the virus. The present contacting the virus reducing the virus represent a rheeus monkey thete defensin anti-viral peptide, which is given in the exemplification of the present invention
 Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.
 New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
 /note= "Linked to amino acid at position 18 to form a
 Tack
 ..
 Query Match 76.8%; Score 86; DB 5; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0058; Matches 12; Conservative 2; Mismatches 4; Indels
 Mccray PB,
 Roller R,
 RC-101/103 retrocyclin peptide analogue.
 Location/Qualifiers
 Disclosure; Page 10; 65pp; English.
 Stinski M,
 Ą.
 1 GVCRCLCRRGVCRCLCRR 18
 1 GFCRCICTRGFCRCICTR 18
 AAE33865 standard; peptide; 18
 30-JAN-2001; 2001US-0265270P.
01-AUG-2001; 2001US-0309368P.
 (IOWA) UNIV IOWA RES FOUND
 (first entry)
 Stapleton J,
 WPI; 2002-674815/72
 Misc-difference
 Sequence 18 AA;
 Unidentified
 16-APR-2003
 AAE33865;
 Maury W,
 RESULT 39
 AAE33865
 LIBXSXEXEXEXEXEX
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 The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
 Anti-viral, viral infection, theta-defensin, lipid environment, amphipathic alpha-helical structure, virucide, anti-HIV, immunisation, viral growth inhibitor, viral proliferation inhibitor.
 Gaps
 cyclic, bacterium; fungus; protozoan; food preservative; analogue.
 Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
 ó
 Score 86; DB 4; Length 18;
Pred. No. 0.0058;
2; Mismatches 4; Indels
 Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.
 Ouellette AJ;
 ABP53295 standard; peptide; 18 AA.
 AAB35046 standard; peptide; 18 AA.
 Claim 15; Fig 16; 110pp; English.
 Theta defensin; antimicrobial; virus; helminth; disinfectant;
 1 GVCRCLCRRGVCRCLCRR 18
 Tang Y, Yuan J,
 10-MAY-2000; 2000WO-US012842.
 99US-00309487.
 Theta defensin SEQ ID NO: 30
 Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
 1 GFCRCICTRGFCRCICTR
 (first entry)
 (first entry)
 (REGC) UNIV CALIFORNIA,
 WPI; 2001-031853/04.
 WO200260468-A2.
 WO200068265-A1.
 Sequence 18 AA;
 Macaca mulatta
 Unidentified
 10-MAY-1999;
 13-NOV-2002
 Selsted ME,
 08-AUG-2002
 27-MAR-2001
 .6-NOV-2000
 AAB35046;
 ABP53295;
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Gaps

RESULT 38 ABP53295

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Monkey, Rhesus theta defensin, RTD-2, antimicrobial peptide, cyclic, antimicrobial; antiinflammatory; antibacterial; virucide, fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.

 18 / Increament of the period of the second o
 Rhesus theta defensin peptide, RTD-2.
 Location/Qualifiers
 Disclosure; Page 24; 72pp; English.
 4;
 ADO35230 standard; peptide; 18
 1 GVCRCLCRRGVCRCLCRR 18
 18-APR-2002; 2002WO-US012353.
 18-APR-2001; 2001US-0284855P.
 Ouery Match
Best Local Similarity 61.1%;
Matches 11; Conservative
 (first entry)
 REGC) UNIV CALIFORNIA
 Waring AJ,
 WPI; 2003-103387/09
 Disulfide-bond 3
Disulfide-bond 5
Disulfide-bond 7
Misc-difference 1
 Sequence 18 AA;
 mulatta
 Disulfide-bond
 WO200285401-A1
 Key
Modified-site
 15-JUL-2004
 31-OCT-2002
 Lehrer RI,
 AD035230;
 Macaca
 RESULT 40
 AD035230
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or sowth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as the respectic agence, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2.
 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 Example 1; SEQ ID NO 2; 46pp; English
 30-APR-2003; 2003US-00427715
 30-APR-2002; 2002US-0377071P
 (REGC) UNIV CALIFORNIA
114
 WPI; 2004-167945/16.
 US2004014669-A1
Disulfide-bond
Disulfide-bond
 MΕ,
 22-JAN-2004
 Selsted
 object
 The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immundeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue
 }
 New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
 /note= "Linked to amino acid at position 1 to form cyclic structure"
 Hong
 structure'
 Cole AM,
cyclic 83. .165. .147. .12
```

ö Gaps ö Match 76.8%; Score 86; DB 8; Length 18; Local Similarity 66.7%; Pred. No. 0.0058; les 12; Conservative 2; Mismatches 4; Indels Query Match Best Loc Matches

Sequence 18 AA;

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Gaps

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Score 86; DB 6; Length 18; Pred. No. 0.0058; 4; Mismatches 3; Indels

à d Search completed: October 26, 2004, 15:34:54 Job time : 115 secs

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